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<p>(21) International Application Number: PCT/US98/06956</p> <p>(22) International Filing Date: 10 April 1998 (10.04.98)</p> <p>(30) Priority Data: 08/837,312 10 April 1997 (10.04.97) US</p> <p>(71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US).</p> <p>(72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US).</p> <p>(74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).</p>			<p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p><b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i></p>
(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs)			
(57) Abstract			
Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.			

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## SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

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FIELD OF THE INVENTION

The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

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Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

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Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

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Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted

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proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

#### SUMMARY OF THE INVENTION

5       The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

20 In other embodiments, the present invention provides an isolated polynucleotide  
 consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

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 NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID  
 NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;  
 25 or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described polynucleotides.

#### DETAILED DESCRIPTION

30 The nucleotide sequences of the sESTs of the present invention are reported in the  
 Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each  
 SEQ ID NO: in the Sequence Listing.

Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

	1	BK8	32	62	DY307	93	DY611
5	2	BV216	DW1001	63	DY643	94	EC259
	3	BV274	33 DW831	64	DY656	95	DY711
	4	BV48	34 DW859	65	DY675	96	EC248
	5	DN351	35 DW875	66	DY988	97	EC32
	6	DN381	36 DW888	67	DY992	98	DO703
10	7	DN405	37 DW901	68	DY225	99	DO713
	8	DU651	38 DW902	69	DY236	100	DR294
	9	DU660	39 DW904	70	DY242	101	DY1
	10	DU675	40 DW905	71	DY254	102	DY10
	11	DU684	41 DW906	72	DY914	103	DY106
15	12	DD364	42 DW929	73	DY946	104	DY117
	13	DD379	43 DW981	74	DY955	105	DY148
	14	DD389	44 DX191	75	DY959	106	DY167
	15	DD401	45 DX219	76	DY961	107	DY17
	16	DD413	46 DX245	77	DY981	108	DY174
20	17	DD426	47 DX256	78	DY357	109	DY175
	18	DD428	48 DX267	79	DY358	110	DY178
	19	DN293	49 DX66	80	DY381	111	DY23
	20	DD454	50 DX81	81	DY413	112	DY27
	21	DD472	51 DY780	82	DY414	113	DY41
25	22	DD475	52 DY803	83	DY415	114	DY42
	23	DT306	53 DY809	84	DY431	115	DY8
	24	DW282	54 DY814	85	DY433	116	DY93
	25	DW300	55 DY261	86	DY436	117	EB107
	26	DW303	56 DY264	87	DY543	118	EB113
30	27	DW323	57 DY266	88	DY565	119	EB163
	28	DT258	58 DY271	89	DY585	120	EB25
	29	DW246	59 DY287	90	DY331	121	EB77
	30	DW324	60 DY297	91	DY586	122	EC172
	31	DW333	61 DY306	92	DY696	123	EC302

	124	EC317	158	EJ90	192	EJ224	226	EP378
	125	EC328	159	EM270	193	EJ240	227	EP38
	126	EC341	160	EM278	194	EJ254	228	EO109
	127	EC349	161	EN186	195	EJ258	229	EO120
5	128	ED105	162	EN215	196	EJ265	230	EQ166
	129	ED21	163	EN217	197	EJ280	231	EQ187
	130	ED23	164	EN234	198	EJ285	232	EQ188
	131	ED30	165	EN239	199	EJ307	233	EQ190
	132	ED43	166	EN256	200	EJ38	234	EQ194
10	133	ED54	167	EN260	201	DO235	235	EQ207
	134	EE177	168	EN264	202	DO238	236	EQ208
	135	EE65	169	EN266	203	DO263	237	EQ214
	136	DQ365	170	EN271	204	DO319	238	EQ215
	137	DK393	171	EN274	205	EJ324	239	EQ218
15	138	DK399	172	EN287	206	EN470	240	EQ219
	139	DO1128	173	EN310	207	EN477	241	EQ220
	140	DO1150	174	EN342	208	EN539	242	EQ221
	141	DZ34	175	EN363	209	EP451	243	EQ226
	142	DZ42	176	EN423	210	EO10	244	EQ229
20	143	EE116	177	EH106	211	EO14	245	EQ230
	144	EE93	178	EH145	212	EO48	246	EQ231
	145	DJ387	179	EH166	213	EO58	247	EQ233
	146	DJ402	180	EH167	214	EO60	248	EQ237
	147	DN551	181	EH178	215	EO62	249	EQ261
25	148	DN559	182	EH180	216	EO68	250	EQ272
	149	DN603	183	EH186	217	EO89	251	ER104
	150	DN629	184	EH188	218	EO90	252	ER106
	151	DN631	185	EH189	219	EO92	253	ER128
	152	DO11	186	EH190	220	EO97	254	ER134
30	153	DO118	187	EH203	221	EP108	255	ER174
	154	DO15	188	EH206	222	EP165	256	ER201
	155	DO157	189	EH95	223	EP219	257	ER77
	156	DO19	190	EJ148	224	EP234	258	ER80
	157	EJ53	191	EJ179	225	EP277	259	ER97

	260	ES136	294	ER399	328	FB264	362	FG208
	261	ES306	295	ER408	329	FB38	363	FG265
	262	ES35	296	ER418	330	FB71	364	FG274
	263	ES37	297	ER430	331	FB78	365	FG278
5	264	ES206	298	ER471	332	FC12	366	FG281
	265	ET13	299	ER476	333	FB349	367	FG291
	266	ET22	300	ER493	334	FC136	368	FG294
	267	ET39	301	ER496	335	FC170	369	FG340
	268	ET84	302	ER498	336	FD152	370	FG363
10	269	EF121	303	ER524	337	FE141	371	FG372
	270	EF129	304	EW13	338	FE5	372	FG380
	271	EF45	305	EX25	339	FD131	373	FG401
	272	EF48	306	EX53	340	EC425	374	FG99
	273	EF5	307	EY165	341	EC428	375	FI203
15	274	EF88	308	EY29	342	ED204	376	FE311
	275	EG194	309	EZ35	343	ED205	377	FE315
	276	EG251	310	EZ4	344	ED210	378	FE322
	277	EH12	311	EZ88	345	ED223	379	FE329
	278	EH213	312	EZ93	346	DI301	380	FE341
20	279	EH22	313	FA8	347	DI303	381	FE366
	280	EH221	314	EV234	348	DI310	382	FE375
	281	EH248	315	EW101	349	DI39	383	FE412
	282	EH29	316	EW109	350	DJ90	384	FE415
	283	EH61	317	EW150	351	DM290	385	FE442
25	284	EH68	318	EY197	352	DM304	386	FE472
	285	EH78	319	EY206	353	DN618	387	FE557
	286	EH80	320	EY215	354	DN896	388	FE568
	287	ER311	321	EZ209	355	DN904	389	FE619
	288	ER329	322	FA139	356	FG119	390	FE676
30	289	ER343	323	FA171	357	FG126	391	FE682
	290	ER366	324	FA252	358	FG140	392	FF150
	291	ER369	325	FA28	359	FG193	393	FF153
	292	ER381	326	FA316	360	FG197	394	FF168
	293	ER395	327	FA95	361	FG198	395	FF175

	396	FF181	430	FH17	464	FN203	498	FO201
	397	FF46	431	FH170	465	FN228	499	FO209
	398	FF49	432	FH24	466	FN229	500	FO211
	399	FF97	433	FH3	467	FN251	501	FO215
5	400	FG41	434	FH39	468	FN254	502	FO253
	401	FG437	435	FH56	469	FP134	503	FO254
	402	FG441	436	FH6	470	FP14	504	FO261
	403	FG448	437	FH66	471	FP163	505	FO267
	404	FG45	438	FM109	472	FP172	506	FO275
10	405	FG492	439	FM13	473	FP71	507	FO290
	406	FG504	440	FM15	474	FP87	508	FO292
	407	FG565	441	FM150	475	EI118	509	FO316
	408	FG567	442	FM170	476	EI16	510	FO324
	409	FG57	443	FM28	477	EI187	511	FO327
15	410	FG577	444	FM3	478	EI203	512	FO348
	411	FG615	445	FM32	479	EI228	513	FO36
	412	FG625	446	FM36	480	EI231	514	FO38
	413	FG630	447	FM60	481	EI236	515	FO40
	414	FG659	448	FM86	482	EI239	516	FO66
20	415	FG708	449	FM95	483	EI243	517	FO75
	416	FG91	450	FM98	484	EI250	518	FP185
	417	FG884	451	FM99	485	EI255	519	FP193
	418	FG891	452	FN172	486	EI264	520	FP233
	419	FG909	453	FN19	487	EI273	521	FP239
25	420	FG912	454	FN29	488	FO11	522	FP246
	421	FG949	455	FN53	489	FO125	523	FP262
	422	FG952	456	FK199	490	FO128	524	FP268
	423	FG965	457	FK217	491	FO133	525	FP271
	424	FH10	458	FK23	492	FO135	526	FP273
30	425	FH116	459	FK32	493	FO147	527	FQ505
	426	FH123	460	FK59	494	FO152	528	DN647
	427	FH13	461	FK78	495	FO160	529	DN650
	428	FH136	462	FN189	496	FO173	530	DN676
	429	FH149	463	FN191	497	FO182	531	DO94

	532	FR292	566	DN827	600	FY201	634	DU4
	533	FR436	567	DN833	601	FY202	635	DU75
	534	FR451	568	DN834	602	FY243	636	FY386
	535	FR473	569	DN850	603	FY265	637	FY388
5	536	FS10	570	DO913	604	FY316	638	FY398
	537	FS106	571	DO923	605	FY318	639	FY414
	538	FS107	572	DO935	606	FY321	640	GA48
	539	FS143	573	DO938	607	FY354	641	GA63
	540	FS173	574	DO944	608	FY356	642	GA64
10	541	FS28	575	DO949	609	FY421	643	DT382
	542	FS31	576	DO952	610	FY430	644	DT385
	543	FS40	577	DQ12	611	FY455	645	DT388
	544	FV35	578	DT2	612	FY484	646	DT464
	545	FV49	579	DT44	613	FY524	647	DT470
15	546	FV68	580	DT53	614	FY530	648	DT478
	547	FW13	581	DT8	615	FY628	649	DT482
	548	FW64	582	FQ661	616	DQ242	650	DU114
	549	FY127	583	FQ672	617	DQ262	651	DU118
	550	FY136	584	FQ696	618	DQ276	652	DU123
20	551	FY60	585	FR1087	619	DQ285	653	DU133
	552	FY65	586	FR927	620	DQ304	654	DU156
	553	FY72	587	FR938	621	DQ313	655	DU157
	554	DN1112	588	FR980	622	DQ51	656	FZ5
	555	DN1118	589	FV122	623	DQ54	657	FZ87
25	556	DN1122	590	FV131	624	DR628	658	DW181
	557	DN782	591	FV132	625	GU215	659	DW309
	558	DN793	592	FV84	626	FM481	660	DX1
	559	DN795	593	FV85	627	DT117	661	DX15
	560	DN806	594	FV95	628	DT133	662	DX19
30	561	DN809	595	FX115	629	DT139	663	DX22
	562	DN810	596	FX127	630	DT164	664	DX29
	563	DN814	597	FX154	631	DU160	665	DX3
	564	DN815	598	FY187	632	DU164	666	DX4
	565	DN823	599	FY199	633	DU166	667	FZ428

	668	FZ163	702	FZ209	736	GE89	770	GF151
	669	DY474	703	FZ254	737	DY516	771	GF179
	670	FZ139	704	FZ346	738	DY529	772	GF99
	671	FX76	705	GA82	739	DY530	773	GB261
5	672	FX65	706	GA85	740	DY538	774	GC499
	673	FX55	707	GA91	741	DY830	775	GD177
	674	DU536	708	DX299	742	DY857	776	GD7
	675	FZ534	709	DX304	743	EA17	777	GE300
	676	DU515	710	DX309	744	EA36	778	DX179
10	677	DU475	711	DX316	745	GG73	779	DY757
	678	DU462	712	DX328	746	DU544	780	EC392
	679	DU353	713	DX336	747	DU560	781	EE15
	680	DU341	714	DX354	748	DZ109	782	DU408
	681	DU306	715	DX357	749	EA105	783	DU410
15	682	DU278	716	DX359	750	EA106	784	DU416
	683	DU244	717	DX363	751	EA110	785	DU447
	684	DU238	718	DX364	752	EA123	786	DX111
	685	DU236	719	DY478	753	EA46	787	DX112
	686	DU231	720	DY497	754	EA58	788	DX123
20	687	FZ639	721	DY508	755	EA7	789	DX138
	688	GC456	722	EA89	756	EA82	790	DX146
	689	GG126	723	EA9	757	GE361	791	DX153
	690	GG129	724	EA90	758	FZ510	792	DX157
	691	GG152	725	GC52	759	GE387	793	EE4
25	692	GG170	726	GC57	760	GE410	794	FZ676
	693	GG182	727	GC585	761	GE463	795	FZ683
	694	GG217	728	GC74	762	GE466	796	GD309
	695	GG440	729	GE28	763	GE468	797	GD358
	696	GG619	730	GE41	764	GE471	798	GG543
30	697	DX279	731	GE51	765	GE524	799	FX516
	698	DX288	732	GE60	766	GE539	800	FX536
	699	DX290	733	GE68	767	GE548	801	FZ1032
	700	DX295	734	GE80	768	GE549	802	FZ1041
	701	DX298	735	GE82	769	GE99	803	FZ1072

	804	FZ781	838	DD12	872	GP304	906	EM40
	805	GA147	839	DD127	873	GP329	907	EM42
	806	GA284	840	DD177	874	GP338	908	EM58
	807	DY723	841	DD204	875	GP340	909	GF185
5	808	DY737	842	DD207	876	GQ13	910	GF187
	809	DY739	843	DD211	877	GQ18	911	GF196
	810	EC399	844	DD217	878	GQ22	912	GF197
	811	EM254	845	DD504	879	GQ38	913	GF207
	812	FX194	846	DD509	880	GQ40	914	GF209
10	813	FX234	847	DD518	881	GQ56	915	GF212
	814	FX281	848	DD537	882	GQ6	916	GF218
	815	FX317	849	DD541	883	DD312	917	GF221
	816	FX353	850	DD71	884	DD352	918	GF222
	817	FX395	851	DH941	885	EK145	919	GF250
15	818	GA293	852	DQ194	886	EK208	920	GF255
	819	GA321	853	DQ204	887	EK223	921	GF256
	820	GA327	854	DQ215	888	EK234	922	GI28
	821	GB160	855	DQ216	889	EK480	923	GI3
	822	GA132	856	EK423	890	EK491	924	GI30
20	823	GA135	857	EK424	891	EK499	925	GI51
	824	GA205	858	EK450	892	EK571	926	GI63
	825	GB814	859	EL15	893	EK578	927	GI7
	826	GF87	860	DD285	894	EK581	928	GI74
	827	GG687	861	EK598	895	EK591	929	GI88
25	828	GG692	862	EK622	896	DD215	930	GI9
	829	GG694	863	EK626	897	EK634	931	DY874
	830	GG702	864	EK649	898	EL358	932	DY886
	831	GG705	865	GO653	899	EL360	933	DY900
	832	GP23	866	GP107	900	EL387	934	EM358
30	833	GP56	867	GP123	901	EL391	935	EM381
	834	GP61	868	GP168	902	EM111	936	EM386
	835	GP65	869	GP232	903	EM112	937	EM388
	836	DD115	870	GP274	904	EM12	938	EM396
	837	DD119	871	GP297	905	EM125	939	EM397

	940	EM401	974	GT43	1008	HU212	1042	EY290
	941	EM406	975	GT6	1009	HU141	1043	EY304
	942	EM408	976	HR712	1010	HS555	1044	EY313
	943	EM409	977	HR704	1011	HR95	1045	FK295
5	944	EM423	978	HR693	1012	HR906	1046	FK301
	945	EM424	979	HR628	1013	HR76	1047	FK317
	946	FE196	980	HR605	1014	HR753	1048	FK328
	947	FE204	981	EK341	1015	HR731	1049	FK349
	948	FE205	982	EK390	1016	EN116	1050	FK350
10	949	FE207	983	EN108	1017	EM341	1051	FK354
	950	FE215	984	FK235	1018	FJ283	1052	FK365
	951	FE222	985	GK428	1019	FJ307	1053	FQ105
	952	FE227	986	GT56	1020	FJ70	1054	FQ239
	953	FE228	987	FQ562	1021	FM176	1055	FQ360
15	954	FE248	988	FQ605	1022	FM197	1056	FQ45
	955	FE263	989	FQ608	1023	FM205	1057	GU353
	956	FE271	990	FQ609	1024	FM208	1058	GX167
	957	GF296	991	FQ612	1025	FM229	1059	GX183
	958	GN38	992	FS49	1026	FQ419	1060	GX208
20	959	GN45	993	FS87	1027	GX48	1061	GX210
	960	GN60	994	GM101	1028	GX5	1062	FM369
	961	GN68	995	GM103	1029	GX92	1063	FM375
	962	GN82	996	GM114	1030	FM289	1064	FM389
	963	GR286	997	GM129	1031	FM290	1065	FM432
25	964	EN10	998	GM153	1032	FM296	1066	FM459
	965	EN37	999	GM158	1033	FM300	1067	FM462
	966	FK127	1000	GM196	1034	FM312	1068	FM479
	967	FK151	1001	GM243	1035	GU512	1069	GX301
	968	GS26	1002	GM259	1036	GU534	1070	GX336
30	969	GS4	1003	GM266	1037	GU608	1071	GX354
	970	EV391	1004	HV38	1038	GX159	1072	GX361
	971	FG535	1005	HV23	1039	GX97	1073	GX403
	972	FG852	1006	HV199	1040	EW304	1074	GX408
	973	GT28	1007	HV181	1041	EY281	1075	GX418

	1076	GU830	1110	GG3	1144	GN97	1178	HE91
	1077	GU925	1111	HA510	1145	HB443	1179	HF289
	1078	GU940	1112	HA422	1146	HC324	1180	HG444
	1079	GX1031	1113	HA382	1147	HC327	1181	HF137
5	1080	GX496	1114	HA360	1148	HC505	1182	HD706
	1081	GX504	1115	HA249	1149	HC724	1183	HG710
	1082	GX509	1116	HA199	1150	HA1054	1184	HG733
	1083	GX536	1117	HA192	1151	HB1041	1185	HG775
	1084	GX540	1118	GZ568	1152	HB746	1186	HI222
10	1085	GX645	1119	GY520	1153	HB752	1187	HI39
	1086	GX700	1120	GY515	1154	HB975	1188	HH215
	1087	GX730	1121	GY330	1155	HC705	1189	HH357
	1088	GX750	1122	GY307	1156	HA791	1190	HH372
	1089	GX753	1123	HA81	1157	HC1002	1191	HH378
15	1090	GX760	1124	HA73	1158	HC1071	1192	HH390
	1091	GX814	1125	HA29	1159	HC1089	1193	HH396
	1092	GX851	1126	HA24	1160	HC831	1194	HH404
	1093	GX909	1127	HA18	1161	HC986	1195	HH433
	1094	GY102	1128	GZ78	1162	GY72	1196	HI2
20	1095	GY105	1129	GZ70	1163	HG159	1197	HH544
	1096	GY138	1130	GZ7	1164	HG620	1198	HH608
	1097	GY211	1131	GZ496	1165	HD161	1199	HH612
	1098	GX1082	1132	GZ495	1166	HD353	1200	HH625
	1099	GX1108	1133	GZ485	1167	HD378	1201	HH640
25	1100	GX1140	1134	GZ436	1168	HD417	1202	HH648
	1101	GX1165	1135	GZ420	1169	HD427	1203	HH691
	1102	GX576	1136	GZ378	1170	HD434	1204	HJ120
	1103	GX595	1137	GZ37	1171	HD499	1205	HJ140
	1104	GX606	1138	GY558	1172	HD569	1206	HJ181
30	1105	GX619	1139	GG894	1173	HD627	1207	HJ184
	1106	GG874	1140	GG907	1174	HD648	1208	HJ22
	1107	GG858	1141	GN114	1175	HE111	1209	HJ253
	1108	GG836	1142	GN115	1176	HE142	1210	HJ265
	1109	GG8	1143	GN145	1177	HE178	1211	HJ362

	1212	HJ395	1246	HM372	1280	HO722	1314	HT166
	1213	HJ411	1247	HM380	1281	HO799	1315	HT176
	1214	HJ444	1248	HM422	1282	HO801	1316	HT193
	1215	HJ65	1249	HM444	1283	HO817	1317	HT43
5	1216	HJ674	1250	HM497	1284	HO82	1318	HT81
	1217	HJ705	1251	HM544	1285	HK719	1319	HW149
	1218	HJ81	1252	HM643	1286	HO1077	1320	HW152
	1219	HJ862	1253	HN72	1287	HO1080	1321	HW190
	1220	HJ949	1254	HN78	1288	HO1087	1322	HW204
10	1221	HK10	1255	HO107	1289	HO1143	1323	HW221
	1222	HK26	1256	HO237	1290	HO1176	1324	HW243
	1223	HK60	1257	HO266	1291	HO1183	1325	HW261
	1224	HJ1037	1258	HO277	1292	HO1216	1326	HW368
	1225	HJ968	1259	HO283	1293	HO1271	1327	HW74
15	1226	HJ981	1260	HO292	1294	HO1329	1328	HX10
	1227	HJ994	1261	HO294	1295	HO1434	1329	HX102
	1228	HJ995	1262	HO305	1296	HO1441	1330	HX110
	1229	HK189	1263	HO315	1297	HO1453	1331	HX113
	1230	HK234	1264	HO332	1298	HO854	1332	HX155
20	1231	HK650	1265	HO358	1299	HO868	1333	HX188
	1232	HK658	1266	HO476	1300	HP262	1334	HX29
	1233	HK669	1267	HO481	1301	HQ36	1335	HX50
	1234	HK713	1268	HO502	1302	HQ72	1336	HY13
	1235	HK899	1269	HO54	1303	GM16	1337	HY3
25	1236	HE187	1270	HO60	1304	GM286	1338	HY55
	1237	HK162	1271	HO600	1305	GM295	1339	HY57
	1238	HL25	1272	HO617	1306	GM335	1340	HZ15
	1239	HL380	1273	HO640	1307	GM365	1341	HZ8
	1240	HL73	1274	HO663	1308	HR397	1342	IA1
30	1241	HM50	1275	HO688	1309	HR560	1343	IA21
	1242	HM54	1276	HO692	1310	HR593	1344	IA32
	1243	HM91	1277	HO693	1311	HR598	1345	IA36
	1244	HM236	1278	HO703	1312	HT13	1346	IB2
	1245	HM280	1279	HO717	1313	HT137	1347	IC2

	1348	IC9	1382	IA167	1413	HW786	1447	IE362
	1349	HY229	1383	IA183	1414	HW810	1448	IH32
	1350	HY244	1384	IA188	1415	HW846	1449	II113
	1351	HY344	1385	IA200	1416	HW849	1450	IJ101
5	1352	HY370	1386	IA220	1417	IB15	1451	IJ163
	1353	HY374	1387	IA64	1418	IB19	1452	IJ167
	1354	HY404	1388	IA69	1419	IB22	1453	IF28
	1355	HY419	1389	IA86	1420	IB28	1454	IF376
	1356	HY435	1390	HW936	1421	IB36	1455	IF456
10	1357	HZ103	1391		1422	IB49	1456	IF87
	1358	HZ109	HW1017		1423	IC103	1457	IJ1201
	1359	HZ111	1392		1424	IC126	1458	IJ1220
	1360	HZ115	HW1044		1425	IC132	1459	IJ1237
	1361	HZ71	1393		1426	IC142	1460	IJ1240
15	1362	HZ76	HW1059		1427	IC155	1461	IJ1247
	1363	HZ88	1394	HW430	1428	IC54	1462	IJ1287
	1364	HW115	1395	HW432	1429	IC87	1463	IJ1292
	1365	HW128	1396	HW440	1430	IC92	1464	IJ1299
	1366	HW477	1397	HW456	1431	IE146	1465	IJ583
20	1367	HW483	1398	HW518	1432	IE147	1466	IJ592
	1368	HW491	1399	HW591	1433	IE149	1467	IJ597
	1369	HW499	1400	HW598	1434	IE169	1468	IJ629
	1370	HW507	1401	HW627	1435	IZ6	1469	IJ638
	1371	HZ116	1402	HW646	1436	JE33	1470	IJ640
25	1372	HZ162	1403	HW649	1437	JE44	1471	IJ642
	1373	HZ185	1404	HW693	1438	JE52	1472	IJ686
	1374	HZ201	1405	HW695	1439	IE10	1473	IG25
	1375	HZ224	1406	HW697	1440	IE47	1474	IG35
	1376	HZ262	1407	HW711	1441	IE73	1475	IH40
30	1377	IA106	1408	HW715	1442	JA37	1476	IH54
	1378	IA110	1409	HW730	1443	JA78	1477	IJ288
	1379	IA114	1410	HW732	1444	JB12	1478	IJ76
	1380	IA153	1411	HW741	1445	JB23	1479	IF292
	1381	IA157	1412	HW750	1446	IE352	1480	IF513

	1481	IF548	1515	IQ58
	1482	IJ1043	1516	IS488
	1483	IJ1048	1517	IS564
	1484	IJ1054	1518	IT23
5	1485	IJ1088	1519	IT44
	1486	IJ777		
	1487	IJ887		
	1488	IJ907		
	1489	IJ928		
10	1490	IJ942		
	1491	IL1		
	1492	IL100		
	1493	IL112		
	1494	IL28		
15	1495	IK11		
	1496	IK14		
	1497	IK20		
	1498	IK203		
	1499	IK209		
20	1500	IK212		
	1501	IK343		
	1502	IK73		
	1503	IO134		
	1504	IO138		
25	1505	IO151		
	1506	IO202		
	1507	IO209		
	1508	IO31		
	1509	IO356		
30	1510	IO420		
	1511	IO62		
	1512	IQ15		
	1513	IQ45		
	1514	IQ55		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification  
5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that  
10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making  
15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the  
20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions,  
25 most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>2</sup>	Hybridization Temperature and Buffer <sup>1</sup>	Wash Temperature and Buffer <sup>1</sup>
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	< 50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	< 50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
15	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

‡: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log [Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

5 A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

10 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any  
15 bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

20 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of  
25 expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting  
30 expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl or Cibacrom blue 3GA

Sepharose ; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which  
5 will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently  
10 purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or  
15 all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic  
20 animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are  
25 known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological  
30 processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

### USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention  
5 may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

#### Research Uses and Utilities

10 The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or  
15 which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding  
20 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related  
25 DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-  
30 DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligand.. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

- and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -
- 5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:
- 10 *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.
- 15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune
- 20 suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may
- 25 be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,
- 30 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other  
5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune  
10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from  
15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing  
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys  
25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the  
30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5 The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci  
10 USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating  
15 autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B  
20 lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of  
25 well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

30 Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient  
5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding  
10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably  
15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor  
20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection  
25 *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or  
30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected  
5 with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured  
10 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-  
15 3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa  
20 et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching  
25 (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

30 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet  
 5 transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post  
 10 irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al.,  
 20 Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic*  
 25 *Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994;  
 30 Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

#### Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

10 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma  
15 induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of  
20 progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the  
25 protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein  
30 may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or  
5 progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural  
10 cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized  
15 neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from  
20 chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

25 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of  
30 fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured  
5 by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

10 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

15 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention,  
20 alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may  
25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

5       A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide  
10 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

15       A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20       The activity of a protein of the invention may, among other means, be measured by the following methods:

25       Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al. Eur. J. Immunol. 25: 1744-1748; Gruber et al.  
30 J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A  
5 protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

10 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors  
20 involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.  
25 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those  
30 described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or  
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality,  
15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### Tumor Inhibition Activity

20 In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor  
25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

30

#### Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

20

### **ADMINISTRATION AND DOSING**

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5           The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. 10           Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15           As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, 20           administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

          In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a 25           mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either 30           simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous  
5 administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an  
10 adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain  
15 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

20 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical  
25 composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers,  
30 antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also  
5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and  
10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices  
15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such  
20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
B	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1 or 2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	Peripheral Blood Mononuclear Cell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	Salivary Gland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	Peripheral Blood Mononuclear Cell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
HO	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
IE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
II	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth  
McCoy, John  
LaVallie, Edward  
Racie, Lisa  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
Agostino, Michael
- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1519
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: Massachusetts
  - (E) COUNTRY: U.S.A
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy Disk
  - (B) COMPUTER: IBM PC Compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Brown, Scott A.
  - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8224
  - (B) TELEFAX: (617) 876-5851

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

GGAGATGTTG AGGTGGCTGC TGACCTGGG TCTCATCTCC TTGATTTTCT TTATCTTCTT      60
CATTGCCGTC CTCTCTAGGC TGTCTPTGGC GAGGAGGGCC CCTGCGGAAT CGTGGTCTAT      120
ATCCCGGATA CATATTCTGC CTCCTGGTTC TACCTTGTTT TCCTGCACCC TGGTTGTCAG      180
CACCTCCAT CACTTCTCCC TGCACAGGAG GGTGGAATA CTGTGGTCTGA CGCCCATAGG      240

```

GTCTCCGCAT GTAGTAAGGT GGGAACTTC GCCTGCGGTA GGGCCGGCGT TGTGGGCCT 300  
 GGCCTTCGGG AGCACTCTCC GATCCCTCGT TCTTTTCCCC ACTCTCACTA TTCTGGTAAT 360  
 TTTGCTGGTA ATTGCGTGA GGAGAACAGG TAGACTCGAG 400

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTAGTTG CCAGCACTTT AAAAATTGGT ATAGTTCACA TAAATATTCT GAATTCAGGC 60  
 TTTTGAAAA GTTGTGGACC CAAGAATACT AGGCCCGCAT TTTCTTACGT CAACATTCTT 120  
 TCCAGGATGA TGAATGGACT GTTCTCTTTG GCCCCTATC TCGAG 165

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCTAGA CCTTCCTCTC CTAATCCCTT CCTTAGGCTC CTGAACCTGT TTGCTCCTAA 60  
 ATCTTGTTAA TTCTTTTCT CTGGATTGT GTTCTTTTG GCTTCCCTT GCCTCCCCCT 120  
 TTCTCTGCT CCAACACTCT TCCCCATGT CTTCTGGCT GTCTCTATGT TCCTCTTCTC 180  
 TTATCCTCAA CTTTCTGTCC ATTGGGCGCT CCTCCCACC TCCCACGCC CAGCCCCTCC 240  
 CTCCTTGGTC TCCTTTTGA TATGCCAAAC CAATTTGGG TCGAGTCAT TCCCTCGAG 299

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGATTGAAT TCTAGACCTG CTTGGATTGC CTTCTGTTGT GGTAGACAAA TCACCATTAA 60  
 ATGACTAAGT TTCACTGTTT TATGTGTTAA TGATCCTTAA TAACAAAAAG TTTTAAAGTC 120  
 TTAATTTCTG AAGATTATGT AAAGGTTAAG AAAGAAATTT TAAGTGAAAA TGATAAAACC 180  
 AAGCAAATGT TTATTAGTTC AATTGTTTTT CTTTTATCT TGCAGCAACG CACATCTCGA 240  
 G 241

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GAATTCGGCC TTCATGGCCT AGGAAATGAC TTTATTGTGG TTGAATTAGT TAAAGGGTAC      60
TTACATTACG TGTTTGATTT GGGAAATGGT GCTAACCTCA TCAAAGGAAG CTCAAATAAA      120
CCTCTCAATG ACAATCAGTG GCACAACGTG ATGATATCAA GGGACACCAG CAACCTCCAC      180
ACTGTAAAGA TTGACACAAA AATCACAACG CAAATCACCG CCGGAGCCAG GAACTTAGAC      240
CTCAAGAGTG ACTTATATAT AGGAGGAGTA GCTAAAGAAA CATACAAATC CTTACCAAAA      300
CTGTACATG CCAAAGAAGG CTTTCAAGGC TGCCTGGCAT CAGTTGATTT AAATGGACGG      360
CTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

GAATTCGGCC TTCATGGCCT ATAAAATTTA AAAATGCTAA GGATCTGGCC CCACAGGCCC      60
CAAAGCTTTT ACAGAGCTCC TCTTAGACAT GAAGATGCCC ATTGGCCTCC TAGGTCCCAG      120
GAGGTGTGGG CAGGACTGCC CTTCTCCGT TCTCATTGCG GGGCTCCTGA AGGGGGTATC      180
TGAAAGTATG TAAATCTGAT GGGAGGTCTG ATCTCCTTT TGCTAGCCCC TGAACCTGT      240
GGTGGAGTCT GGCTGATGGC CAGGGCCATG TCCTAGAGGG GACTCCCTG CAGGAGGCGG      300
GCTCTAAAGG GAGTGGTGTG CCTTTAGGCC AGGGTTCACA GTCGGGGTGG TCTGGAGACT      360
GCAGGACTCA GGGCCTGGGG GTGGCATCAG TCTGGCCAGG CCCTGCGTCA CTGTCACCCA      420
CTGTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

GGGTGGCTCA TGCCTGTAAT CCCGGCACTT GGGTAGGCCA GGGCAGCAGG ATCGCTTGAG      60
CCCGGGAGTT CGAGACAGCC TGGGCAACAT GGTGAGACCC TGTCTCCATA AAATTTTTTA      120
AAAAATTGCC AGGTGTGGTC GTGTGTGCCT GTGAGGCTGA GGTGGGAGGC TCGCTTGAGC      180
CCAGGGGTCA AGGCTGCAGT GAGCCATGAC TGCACGCCAC TGCACTCCAG CGTGGGTGAC      240
AGAGTGAGAT ACTGTATAAA AAAAAAAGC TAAAACAAA CAAGAAGTAT TATCTTAAGC      300
ATGTTATTTA GAAATATGGA GATAAATAAA AATAACTGAA AGTAGTCGT TGCTTCTGAG      360
GAGAGAAATT GGGAGTTGGC AAGGTCTCGA G

```

(2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

GCTTTTGGAG CTGCTAAAT GCCGGATTAC CTCGGTGCCG ATCAGCGGAA GACCAAAGAG      60
GATGAGAAGG ACGACAAGCC CATCCGAGCT CTGGATGAGG GGGATATTGC CTTGTTGAAA      120
ACTTATGGTC AGAGCACTTA CTCTAGGCAG ATCAAGCAAG TTGAAGATGA CATTGAGCAA      180
CTTCTCAAGA AAATTAATGA GCTCACTGGT ATTAAGAAT CTGACACTGG CCTGGCCCCA      240
CCAGCACTCT GGGATTGGC TGCAGATAAG CAGACACTCC AGAGTGAACA GCCTTTACAG      300
GTTGCCAGGT GTACAAAGAT AATCAATGCT GATTCGGAGG ACCCACTCGA G              351

```

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

GTGATGTGTC ACCCAAGTG CTCCAGTGC TTGCCAGCCA CTTGCGGCTT GCCTGCTGAA      60
TATGCCACAC ACTTCACCGA GGCCTTCTGC CGTGACAAA TGAAGTCCCC AGGTCTCCAG      120
ACCAAGGAGC CCAGCAGCAG CTGACACCTG GAAGGGTGGG TGAAGGTGCC CAGGAATAAC      180
AAACGAGGAC AGCAAGGCTG GGACAGGAAG TACATTGTCC TGGAGGGATC AAAAGTCCTC      240
ATTTATGACA ATGAAGCCAG AGAAGCTGGA CAGAGGCCGG TGGAAGAATT TGAGCTGTGC      300
CTTCCCGACG GGGATGTATC TATTCATGGT GCCGTTGGTG CTCCAAACT CGAG              354

```

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

GAATTCGGCC TTCATGGNCT AGGAGGAGGA AGAGGAGTAC GAGGATGACG AGGGAGGAGG      60
GGGAAGACGA GGAGGAGGAG GAGGCTGCGG CAGAGGCTGC CGCGGGGGCC AAACATGACG      120
ATGCCACCGC CGAGATGCCT GATGACGCCA AGAAGTAAGG GGGGCAGAGA TGGATGAAGA      180
GAAAGCCAC GAAGAAAAA GCCTGGTTTT GTTTTCCCA GAATATCGAT GGAATTAATA      240
AGGCTCAGGT TTTTGACCAA AATACAATGT GAATTTATTC TGACATTCCT AAAATAGATT      300
AAATTAAAGC AATTAGATCC TGGCCAGCTC GATTCAAATT TGACTTTCAT TTTGAACATA      360
ATAAATATAT CAAAAGGTGT TAAAGAAAAC TGAATTAAAC CCAAAATTAT GTTTTCATGG      420
TCTCTCCTCG AG              432

```

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 687 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

CTATTTTACA TGCCACCAG CATTGTATGG GGCTTCTCAC TTGTCCACAT GCTTGCTGT      60
GTCATATTTG ACTTAAAGCT TATTTTGACG GGAAACCAAT TTGTCCTTTT TTTGGAAAG      120
GATGGCACCA CAGATGTGAC GCGGACAATG CATTITGGGA CCCCTACAGC CTACGAGAAG      180
GAATGCTTCA CATATGTCTT CAAGGGCCAC ATAGCTGTGA GTGCAGCCGT TTTCCCGACT      240
GGAACCAAAG GTCACCTTCT TGACTCCTTT GCCCGTTCAG CTTTATGGGA TTCAGGCCTA      300
GATTACTTGC ACGGGACTGG ACATGGTGTT GGGTCTTTTT TGAATGTCCA TGAAGTCTCT      360
TGCGGCATCA GTTACAAAAC ATTCTCTGAT GAGCCCTTGG AGGCAGGCAT GATTGTCACT      420
GATGAGCCCG GGTACTATGA AGATGGGGCT TTTGGAATTC GCATTGAGAA TGTGTCTCTT      480
GTGGTTCTCTG TGAAGACCAA GTATAATTTT AATAACCGGG GAAGCCTGAC CTTTGAACCT      540
CTAACATTGG TTCCAATTCA GACCAAAATG ATAGATGTGG ATTCTCTTAC AGACAAAGAG      600
TGCAGCTGGC TCAACRAATTA CCACCTGACC TGCAGGGATG TGATTGGGAA GGAATTGCAG      660
AAACAGGGCC GCCAGGAAGC TCTCGAG                                     687

```

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

GAATTCGGCC TTCATGGCCT AGTCGGTGGG TGCCTGTAGT CCCAGCTACT TGGGAGGCTG      60
AGGGAGGAGA ACTGCTTGAA CCGGGAGGC AGAGGTTGCA GTGAGCCGAG ATTGTGCCAC      120
TGTACTCCAG CCTGGGCCAC AAAGCAAGAA TCTGTCTCAA AAAAAAAAAA AAGAAAAGAA      180
AAGAATAAAT TTCTTTTCCC CTGAAGAAG TTGATTTAGG CACAGACTCT GGACTCTGGA      240
TTTCCCAACA TGTCTTATCT AGTCAACTCA AGTATCTGGA CTACAATTTT CTTGAAAGCA      300
AAGCCCATAT ATTAATAATC TTTACTTGTA TATAAATATT CAATAAATCA TTAAGTAAAT      360
GTGTAGAAGA ATTTTATGCT CAATAAGATC CACCCGATCA TGCATTTGAA AATTCTCGAG      420

```

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

GAATTCGGCC TTCATGGCCT AGCACATACT CTGCTTTTCT GTCAACATCC CATTITGGGG      60
AAAGGAAAAG TCATATTTAT TCCTGCACCC CAGTTTTTTA ACTTGTCTC CCAGTTGTCC      120
CCCTCTTCTC TGGGTGTAAG AAGGGAAATT GGAAAAAAA TTATATATAT ATTCTCCTTT      180
TAATGGTGGG GGGCTACTGG AGAGGAGAGA CAGCAAGTCC ACCCTAACTT GTTACACAGC      240

```

ACATACCACA GGTTCCTGGAA TTCTCATCTT CGAACCTAGA GAAATAGGTG CTATAAACAG	300
GGAATTAAGC AAAATGCTGG ATGCTATAGA TCTTTTAATT GTCTTAATTT TTTTCTATT	360
ATTAAACAAC AGGCTCGAG	379

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTCATGGCC TACGGAAAGT CAGCATGGAT AACAGACTGA TGGAACCTCTT TCCTGCCAAT	60
AAGCAAAGTG TTGAACACTT CACAAAATAT TTTACTGAGG CAGGCTTGAA AGAGCTTTCA	120
GAATATGTTT GGAATCAGCA AACCATCGGA GCTCGTAAGG AGCTCCAGAA AGAACTTCAA	180
GAACAGATGT CCCGTGGTGA TCCATTTAAG GATATAATTT TATATGTCTA GGAGGAGATG	240
AAAAAAAACA ACATCCCAGA GCCAGTTGTC ATCGGAATAG TCTGGTCAAG TGTAAATGAGC	300
ACTGTGGAAT GGAACAAAAA AGAGGAGCTT GTAGCAGAGC AAGCCATCAA GCACTTGAAG	360
CAATACAGCC CTCTACTTGC TGCCTTTACT ACTCAAGGTC AGTCTGAGCT GACTCTGTTA	420
CTGAAGATTG AGGAGTATG CTATGACAAC ATTCATTCA TGAAAGCCTT CCAGAAAATA	480
GTGGTGCTTT TTTATAAGC TGAAGTCCTG AGCGAGGATG CCCTCGAG	528

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCC TTCATGGCCT AGCCCAGGCC ACGCTACACT CTGCCCACAC TGGTGAGCAG	60
GAGGTCTTCC CACGCCCTGT CATTAGGCTG CATTACTCTT TGCTAAATAA AAGTGGGAGT	120
GGGGCGTGCG CGTTATCCAT GTATTGCCTT TCAGCTCTAG ATCCCCCTCC CCTGCCTGCT	180
CTGCAGTCGT GGGTGGGGCC CGTGCGCCGT TTCTCCTTGG TAGCGTGCAC GGTGTTGAAC	240
TGGGACACTG GGGAGAAAGG GGCTTTCATG TCGTTTCCTT CCTGCTCCTG CTGCACAGCT	300
GCCAGGAGTG CTCTGCCTGG AGTCTGCAGA CCTCAGAGAG GTCCCAGCAC TGGCTGTGGC	360
CTTTCAGGTG TAGGCAGGTG GGCTCTGCTT CCCGATTCCC TGTGAGCGCC CACCCTCTCG	420
AAAGAATTTT CTGCTTGCCC TGTGACTGTG CAGACTCTGG CTCGAG	466

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCC	TTCATGGCCT	AGCGTGATCC	TGGAACGTGC	TCTAGTTCGA	GAGAGTGAGG	60
GCTTTGAGGA	GCATGTACCA	TCTGATAACT	CTTGAAGATA	CAGAGAGAAA	TCCATCTTTT	120
CCCAGGTCTC	CTTCACTGAA	AACAAAAATC	TACTTACATA	CACTGTCACC	TTAGCATCAG	180
AGTCGGATTA	ATGAAGTCCG	GAACAAGAGG	TTGTGAGAAT	CTAAGATGGA	ACCTTTCTTT	240
CTTCTTTCT	TTTTTTTAA	ATTTGTATT	TTCCATCCAA	CACTCGAG		288

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCC	TTCATGGCCT	AGGGCTCTGC	TTATAAACTT	CAAAGTTACA	CTGAAGGATA	60
CGGTAAAAAC	ACCAGTTTAG	TAACCATTTT	TATGATTGG	AATACCATGA	TGGGAACATC	120
TATACTAAGC	ATTCTTGGG	GCATAAAACA	GGCTGGATTT	ACTACTGGAA	TGTGTGTCAT	180
CATACTGATG	GGCCTTTTAA	CACTTTATTG	CTGCTACAGA	GTAGTGAAAT	CACGGACTAT	240
GATGTTTTCA	TTGGATACCA	CTACCTGGGA	ATATCCAGAT	GTCTGCAGAC	ATTATTTCCG	300
CTCCTTTGGG	CAGTGGTCGA	GTCTCCTCTT	CTCCTTGGTG	TCTCTCATTG	GAGCAATGAT	360
AGTTTATGG	GTGCTTATGT	CAAAITTTCT	TTTTAATACT	GGAAAGTTTA	TTTTTAATTT	420
TATTCATCAC	ATTAATGACA	CAGACACTAT	ACTGAGTACC	AATAATAGCA	ACCCTGGTCT	480
CGAG						484

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTGGCCT	TCATGGCCTA	GGAGATATAC	CTAATGCTAG	ATGATGAGTT	AGTGGGTGCA	60
GCGCACCAGC	GTGGCACATG	TATACATATG	TAACTAACCT	GCACAATGTG	CACATGTACC	120
CTAAAACCTA	AAGTATATAT	AAAAAAAAAA	GACNTCGCTA	GTGAGCACGC	TGTATACGAC	180
ATCGCTAATG	AGGACACCAT	ACAAGGCATC	GCTAACGATG	ACGCTGTACA	CAACATCACT	240
AATGATGACA	CCGTATAAGA	CATCGCTAAT	TATGACGCTG	TATACGACAT	CGCTAATGAC	300
ACCGTACGAG	GCACGCTAAC	AAGGATGCTG	TACACAACAT	CGCTAATGAG	GACAGTGTAC	360
AAGCCATCGC	TAATGAGGAC	ACTGTATATG	ACATTGCTAA	CGAGGACACT	GTACAAGGCA	420
TTGCTAACGA	GGACGCTGTA	CACAACATCG	CTAATGACAC	CATATAAGAC	ATCACCAATG	480
AGGATGCTGT	ATATGACATC	GCTAATAACA	CCGCTCGAG			519

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCAGCTCTCA TCCTCGTCTC CCCAACACCA TAACGTCTCTC ATCCCGCCTC CAACCCACAC	60
CAGGCCGAAG CCCTCAGAGA GTGTTTTCAT CAGGAACCAC TCTCGAACCT GAAGGTTGAC	120
TTTAGCGTTT AGCAACCCAG GCGGGTGTGT GTGTTTCCCG TTTTGTITTC TGAGTGGTAG	180
CAGTGATCAC CGTAATTCCA TGTAGCCATG TGCTAGCAGA ACCCCTGTGT CCTCACCGTG	240
GCCCGTGTGA CCCAGCCGA CGAGTGCCCG GCGGAGTCCC CGCTGCCTTC CCATGGTCCA	300
GTGAGCTGCC AGGGCATCAC ATGACTCTCA GCTGGGCTCG AG	342

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCGGCC TTCATGGCCT AGAGCAGCTC TGAGGTAGAA ATTACAACGA TGAAAAGAGC	60
ACAACGTACA AAACCAAGAA AGAGTCTGTT GTGTGAAGGG TCATTTCGATG AAGAAGCTTC	120
TGCACAGTCC TTTCAGGAAG TGTTAAGTCA ATGGAGAACC GGAAATCATG ATGACAACAA	180
GAAACAGAAAT TTACATGCAG CAGTAAAAGA CTCATTGGAA GAATGCGAAG TACAGACTAA	240
TCTGAAAATT TGGAGAGAAC CACTTAATAT TGAACCTAAA GAAGACATTG TATCCTATAT	300
GGAAAAATTA TGGCTTAAAA AACACAGGAG AACTCCACAA GAGCAACTTT TTAAAAATGCT	360
ACCAGATACG TTCCCACATC CACATGAAAC CACTGGTGAT GCACAGTGTT CTCAAAATGA	420
AAACGATGAA GATAGTGATG GTGAGGAGAC CAAAGTACAA CACACAGCTC TTTTATGACC	480
AGTAGAAACA TTAAACATAG AGAGACCTGA ACCATCTCTA AAGATAGTCG AACTGGATGA	540
TACTTATGAA GAGGAATTG AAGAAGCAGA ACATCTCGAG	580

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAATTCGGCC TTCATGGCCT AGAAAGATCT AATTATCATG GACCTGCGAC AGTTTCTTAT	60
GTGCCTGTCC CTGTGCACAG CCTTGCCTT GAGCAAACCC ACAGAAAAGA AGGACCGTGT	120
ACATCATGAG CCTCAGCTCA GTGACAAGGT TCACAATGAT GCTCAGAGTT TTGATTATGA	180
CCATGATGCC TTCTTGGGTG CTGAAGAAGC AAAGACCTTT GATCAGTTGA CACCAGAAGA	240
GAGCAAGGAA AGGTTTGGAA AGATTGTAAG TAAATAGAT GCGACAAGG ATCGGCTCGA	300
G	301

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
GAATTCGGCC TTCATGGCCT AAAAAAAGGA TGGTGTGTTG AGACCAGAAG CAGCAGCAGT    60
CCTCGACATC AACTACAACCT TTCCCTTCGCA CAGTGCATAC CCTCTGATAT ACTGAACCCA    120
ACGCCTATCC TCCAGCCCCC TAAGAACTAG AGAGGGAGCC TCACAACATT CCAATTTAAT    180
CCTTCAGAAA ATTCATTACT CTTCAAAGTT GTCTGTGGTT TTGTGACAAC GATATGACTA    240
GGTGCAAAAT GGCTTGCAAC TAATTAACAA ACATAGAAGC ATCCAACAAA CATATACGTG    300
CACAACTCTGA GGATTTAGGG ATGAAGCTCG AG                                332
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
GAATTCGGCC TTCATGGCCT ACCAGCCTGG GCGACAGAGC AAGACTCAGT CTCAAAACAA    60
AACAAAACAA AACAAAAAGA GAAGGCTATT ATTAACATTC GAGATAATGT GCCAGACTGC    120
TTCCATGTAT TTTCATTATT CTGTCCCAAA TCTGGTGAAG TGGGTATCTG CACAGCTTTC    180
TCTAGATTGA ACAACTAGTA AGGGGGCTGG CCCTGGAGAA AGTTACCTCC TGCTCGAG    239
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
GAATTCGGCC TTCATGGCCT ACTTTTATAT TGTATTATTT GTAAAGCATC TTTTCTTCAA    60
TTCTTGTTGG CATTCTGGGC CAAAATATTT CAGGTTGGTT CGGTGTGGAG TTAAGAAAAG    120
CAGGCGTTTT AGTGGAGAAA TGGGGAACAG CATCAAGAAA GGCTTTTTTTC CTTTTTCTT    180
TTTTTTTTTG AGACAGAGTC TTGCCCTGTC ACCCAGGCTG GAGTGCAATG GTCTCGAG    238
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
GAATTCGGCC TTCATGGCCT AGATGGATTT CTTAATTGAA GTACTTTTAT AATCACAGTG    60
```

ACTGAACAAA ATATTTTCAA AGACATTTGT CATTCTTAA AGCCAAGATT TTAAAGACTA	120
ATGTCCTTCC TGAGGGTTAC TTTACTATAC TGTGTATGGT GTATAGCCAC AGAAAGTCAG	180
TCTGATAAAT TTTCAATGTG TAAGTGTGAT GCATTCAACC CAGATCTCGA G	231

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAATTCGGCC TTCATGGCCT ACACAGAGTA TATTTATAGC TATCTCAGGG TCCTTGTCCTA	60
ATTGTCCTGTG TCATTTCTTC ATCTGCTTCT ACTGATTTT TCTGCTTCTG TTTACTCTTC	120
ATTTTGGACC TATTTTCCCT TATTTGGTGC TTTCATACA ATTTGTTGGG ACTGGATCTT	180
TGCTAGTCCT TTAAATGTTT TTAAGCTTTG TTTTGGGATG CAGTTAGGTG ACTCAGAAAC	240
AATCAGAAAC AATTTGATCC TTTTATGTCT CTTAAGCTTT GTTATAGGCA GGACCAGAGC	300
TCTCGAG	307

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTCGGCC TTCATGGCCT ACAATAATAG CCTCCACCT GGTCTTCCTT CTTCAGTCTC	60
TTTCTCTTTT CCCAAAGCTC TTGAATCCTA CATGAACCCA TGCCTCGGTC AAAATATTAC	120
AGGCTGCAGC CAATCTTCAA GTGGCATAACA GGCCAAACAT CCATTTATAA TATGGTTGGA	180
ATTCTAACA CATTATATCA TAGATCTAAT GCCATACAAT AGGTGGAGGT TAGATCTCTA	240
CGCAACTCTC GAG	253

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCGGCC TTCATGGCCT ACAGAGAACT TGTGTTCCGG TTTATTGAAG TTCAGACACT	60
TCTCCTCGCT CCATTCGTGC CACATTGTGT TGAGCACATC TGGACACTCC TGGGAAAGCC	120
TGACTCAATT ATGAATGCTT CATGGCCTGT GGCAGGTCCT GTTAATGAAG TTTTAATACA	180
CTCCTCACAG TATCTTATGG AAGTAACACA TGACCTTAGA CTACGACTCA AGAAGTATAT	240
GATGCCAGCT CGAG	254

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
GAATTCGGCC TTCATGGCCT ACGAGAAGGA GTGGAAGAGT AAGCAGACTA GGAAAATACA      60
GTACAACCAT CAGGCAGCAT TACAGACCCA CTTAAGGTTT GTGGCCATGT GTGGTTGTGT      120
GGTTTTTTTT CTGGCCATGC TCAGTTACAT AGGGGCAAGT GCAAAAAAAA CCCAGAGTT      180
TGTTTAACT AGAGCTCTGG TTTTGCCAAA C                                211
```

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 521 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
GAATTCGGCC TTCATGGCCT AGGATCAGGT TCGTCCTTTA GTGTTGTGTA TGGTTATCAT      60
TTGTTTGGAG GTTAGTTTGA TTAGTCATTG TTGGGTGGTG ATTAGTCGGT TGTTGATGAG      120
ATATTTGGAG GTGGGGATCA ATATAGGGGG AAATAGAATG ATCAGTACTG CGGCGGGTAG      180
GCCTAGGATT GTGGGGGCAA TGAATGAAGC GAACAGATTT TCGTTCATTT TGGTTCTCAG      240
GGTTTGTAT AATTTTITAT TTTTATGGGC TTGGTGAGG GAAGTAGGTG GTGGAGCACA      300
GGCACTGCAG GTCAATGGAG GTGGAGTACA GGGACTACAG GTCAATGGAG GTGGAGCACA      360
GGGACTAAG GTCAATGGAG GTGGGGCACA GGGACTACAC GTCAGTGGAG GTGGAGTCAC      420
AGGGACTACA GGTCAGTGA GGTGGAGCAC AGAGACTACA GGTCAGTGA GGTGGGGCAC      480
AGAGACTACA GGTCAGTGA GGTGGAGCAC AGAGACCACA G                                521
```

## (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
GAATTCGGCC TTCATGGCCT AAAATTTCTT CTAAGTACTG ATTTAGCTGC ATTGTATAAG      60
TATATGCTTC CATTTCATT CATTCCAAA TATTTCTAA TTTCCTTGC AATTTTTTTT      120
TCAGGAATTC GGGCCTTGCT GTGTGCCCCA GGCTGGAGAG CAGTGCCACT ATCACAGCTC      180
ACTATAAACT CAAACTCCTG GGCTCAAGCA ACCCTCCCAC CTCCCAACTC CCCTCGAC      238
```

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
GGTTTCTTAA AAAAAAAAAA AAAAGGAATT TGATCCAGAG CAATTTTCT CAATTAAAT      60
TTGTGATTAC ATTTCTGAGT TTCCATGGCA GAGTTGTGAG TGGGGCTGTG ATATAATTTA    120
ACTTCTCCTA AATTGCTGAC ACCGATAACC CTATAAATTA ACAGATGGCG GAGGGAAATC    180
TCCTGGCTTC TTCCTGGCTA GTTTTTTTA ATGGTCTGAT TTTGTAATA GGGGTTTGA     240
GTCCCAGCCG ACTCGAG                                         257
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
GAATTCGGCC TTCATGGCCT AAAGACTTAC GTTATATTTT CATATACTCC TTCCCACTCT      60
TAGTGTGTTG TCAATATACA TTTTGTTTTA CATGTAAAAA CACCACAGTA TATTGTTCTT    120
AATTTTGCTT TTAATAGTAA ACTGTCTTAT AACAAATTAT GAAAATGGAA AAAACATGT     180
CTTTCTTATT TGCCCTCATA TTTATCCATT TAGGCACTCT TCCTTTTCC CTTTCATTCC     240
AGGTTCTCGA G                                         251
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
GAATTCGGCC TTCATGGCCT ACTAACATTT ATGAAAATTA TTTGTAAATA AAATAAGAGG      60
CATTGAGATT AAAATTGGAG ATAAAGTTGC TGATGTGTTG TTTTCCTGAA GTATTTTTTT    120
TCTTAATTCT GATCTTTGTT TCCAATACA ATCACACTCA CACCCTTGCA GTTCAGTTTC    180
CTGACGACTC TCTAGTGTGC CAGATCTGTG TTTCTATGTC AGTGATCTGT TCCCACATC     240
TCGAG                                         245
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
GAATTCGCTT CATGGCCTAC CGAGAAATGG GTGTGATTGC TGCCATGAGA GATGGTTTTG      60
GTTTCATCAA GTGTGTGGAT CGTGATGTTC GTATGTTCTT CCACITCAGT GAAATTCTGG      120
ATGGGAACCA GCTCCATATT GCAGATGAAG TAGAGTTTAC TGTGGTTCCT GATATGCTCT      180
CTGCTCAAAG AAATCATGCT ATTAGGATTA AAAAAGTTCC CAAGGGCAGG GTTTCATTTC      240
ATTCCCATTC AGATCACCGT TTTCTGGGCA CGGTAGAAAA AGAAGCCACT TTTTCCAATC      300
CTAAAACCAC TAGCCCAAAT AAAGGCAAAG AGAAGGAGGC TGAGGATGGC ATTATTGCTT      360
ATGATGACTG TGGGGTCTC GAG                                         383
```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
GAATTCGGCC TTCATGGCCT ACTGCCGCTC CTGGTGCTGC TTGTGTGCTC GTTTGGTGCG      60
GACCTGGTAC CTCITTTGTG AAGCGGCAGC TGAGGAGACT CCGGCGCTCG CCATGGCCGA      120
CGAAAAGCTC GAG                                         133
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
GAATTCGGCC TTCATGGCCT AAGGTAGTCT AGGCTCATCT TCATGAGGGA ACTGAGGTCT      60
TGGGGGGTGG GGGTTACCCA AATAGGTTCA CAGAAGAACC AGAAATAAAA CCTGCCITTC      120
TAGACTGTAA GTCTTGATGTGATGTCATCTAA ATGGTTGTCT CTATACAGCA ACTCATCTCT      180
AGAACTGAAA ATAAGTTTAA ATCCCTCCTC CATCCCCAAT AATCAAGCT GCATTTGAGA      240
GAAAACCCAG ACTTTGGAAT CAGACAGCAA CTCGAG                                         276
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTTGTGC TCTTAGAGTA GGAGTTGGAA CTATAGGACT TGAAGGCAAG AGCAGGTATC	60
TTATCAAGGA TCTACTCACT CAGTTTCCCT AAAGCTCTCT CTCCAGATCG GATTCAACCG	120
CACATCATGA CAGATGTTC GGCTACATTT ACCCAGGCTG AGTGTAAATGG GGATAAACCA	180
CCTGAAAACG GTCAACAAAC AATCACTAAA ATCAGTGAGG AATTGACTGA TGTGGACAGC	240
CCCCTGCCAC ACTACAGGGT AGAACCCAGT CTGGAAGGTG CACTCACCAA AGGAAGTCAG	300
GAGGAAAGAA GAAAATTACA AGGGAACAGA CTCGAG	336

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAATTCGGCC TTCATGGCCT AGTCGGAGAA GGACATCCAG GATCTGAAGT TTGGGGTCGA	60
GCAGGATGTT GATATGGTGT TTGCGTCATT CATCCGCAAG GCATCTGATG TCCATGAAGT	120
TAGGAAGGTC CTGGGAGAGA AGGGAAGAA CATCAAGATT ATCAGCAAAA TCGAGAATCA	180
TGAGGGGGTT CGGAGGTTTG ATGAAATCCT GGAGGCCAGT GATGGGATCA TGGTGGCTCG	240
TGGTGATCTA GGCATTGAGA TTCCTGCAGA GAAGGTCTTC CTGCTCAGA AGATGATGAT	300
TGGACGGTGC AACCGAGCTG GGAAGCCTGT CATCTGTGCT ACTCAGATGC TGGAGAGCAT	360
GATCAAGAAG CCCCGCCCCA CTCGA	385

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATTCGGCC TTGCTAAAAA AAAAAAAAAA GAGGCAAGTA ATGTAATATC CCCACCTTT	60
GGTTTTCTTA TCTATAAATA CTGATTAAAA AAAAAAGTAC ACTGTCTGCC TTATAAGCTA	120
AAATGAGTGA ATACAGGCAA AATGCCTTAC ATTTTACTTT ACATTTACTA AGCACCCAGA	180
AAATGTTAAC TATGATGACA ATTATGATGA TGATGATATT GATATTTTCA AGGAGGGCGC	240
TCGAG	245

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATTCGGCC TTCATGGCCT AAATAAAGAT GATTTTGTG CTTAGCAGTT TAAGGTATAT	60
GGCTGCATAT GCAAACTCT TTCCAATTC AGTCGCTACT TTTACTTCTG CCCTTCTAT	120

CCATCGTCTT CATTTTGTGT GTACAGTGCT GTGTGTAAGC TTATCAGTGT GTTTTTTTAT 180  
 TTGTATCAGT CATGAAAGTC CTGTTAGGTA TCCAGAGTTC TATTTATCTA GCTGTACAGA 240  
 TCTCGAG 247

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGATATGGTA ACTGAGAACC ATTTTCTAGT TGAGATAACT CATGTACAGG GGGGGTCACA 60  
 TGA CTCAACA ACACACAGAG CACAGAAGAG AACCAACAAT CTCGAG 106

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GCGTATTTCC AAGTGATGT ATTTCTAAG ATAGATTTTT TAAAAACAAA AAATCTTAAT 60  
 TTAGATGATA AGCGATTTTT ACCTTTTTTT TTTTTCAAA GCAACTTGAT CCTGTAAGTT 120  
 TTGGCATCTT AAGTGGAAAT GTTCATGCAG TTTTGCTGGA TCTTCGCTAT GGCAGTAAAA 180  
 TGCAATACAG CACTGTGGTT AAGAGTGCAG AACGGAGTCA GTCAGCCTGA ACTCGAG 237

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT AGGGAGTNGG 60  
 TGTGTCGTG CATTTATTG GATCATGGAA GGTGTAGAT GTGTATTCT AACTGTAGAT 120  
 AATGGAGGAC ACATATTTGG GGAGTTTGA GAGGATGTGT ATGTGTGTGT GTGTGCAGTG 180  
 TGGTATTCT CTATGTTTG GTGGGTGGG TATGTATCCA TCAAAATATC TCAGATTATC 240  
 TGATGTAAGA AAATAATTCT GCATCTCAGT GACTTCCAAC AAGGTAGGTT TCTCATGTAT 300  
 GTTATGTGTC CTCCATTGGT TGGCTTTGAT CAGTTACTGG TCCTGTGCCT TGGATCCAGA 360  
 TGGATGAAGC GGCCTCATTT GGGACAGGAC TAGAAGGACT TCTTCTGCTC AGAGTCATAC 420  
 ATGGCATTTT TGATCACATT TCATTGCGCA TAACAAGTCA TGTGGCCATA CTCGAG 476

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAATTCGGCC	TTCATGGCCT	AGGCAAATC	TGCTGGACTT	AACTTCATCA	ATGTAGTGGG	60
CTCTGTTTGT	GGGGCCAGG	CTTTGATGAG	TGGTTCAAAC	CCCATGCTGG	GCTGTAACAC	120
TGGTGCCATA	ACTCCTGCAG	GAATAAACCT	GAGCGGCCTT	CTACCCTCAG	GAGGTCTGCT	180
ACCAAATGCA	CTGCCAGTG	CAATGCAGGC	AGCTTCTCAA	GCAGGTGTTT	CATTGGTTT	240
AAAAAATACT	TCAAGTCTCA	GGCCCTTAAA	TCTACTCCAG	CTTCCAGGTG	GTTCACTTAT	300
TTTAACTACT	CTGCAGCAGC	AGCAACAGCA	GCTCTCCAG	TTTACACCAC	AACTCGAG	358

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTCGGCC	TTCATGGCCT	AATCATTITG	ACTTTCAGTG	CTTTCATGA	CCAGTGGCCT	60
CCAGGGATAA	AGCAACTGCT	TGTTTGCAG	GGCGTCTCT	GCGTGCTGA	GCCATCAGCC	120
TCCAATACGC	CAATGCCCAT	AGATGCTAGT	TACAGCCCTG	CTTCCTCCTA	CATAGGGTTC	180
TGTCATCACT	GAGTCTCACC	ATTCCCTCT	CCCCAGTGTG	TTTATTATGT	GACACACACA	240
CACGGCACTA	TGTTTAAAAA	AGCGTGCTCA	CTGGCAACCT	CTTGGCGTTG	TGTGTTTATT	300
CTGTGTTTITG	TATTGGTGGT	ATCTTGGGGT	CGACCGAAAG	AGTCAACCTC	GAG	353

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAATTCGGCC	TTCATGGCCT	AGGGAGCTAC	CAGATGCTGA	AGAAAGGGCC	CTGGCAGACT	60
GGGTTCAAAC	TCAGCCATTG	TCAGCTTGGT	AACCTTGACC	AAGTGTCTTC	CCCTCTGTGA	120
GCCTCAGTTT	TCTCAATAGT	AAGAGGGGAT	AACACACTTA	CCTCTCATAG	CTGTGGACAT	180
GGAGGTGAAA	GTGCCGCATA	CACTGTAAAG	TGTTATATAC	GTGTAAGAGA	AAAAATCGGG	240
CCAGAGGCTG	GGCTTGTGTT	AATTGATTCA	GGAAATTAC	CAGAGGCCCC	CTAGATGCAA	300
CGTCCCTTTG	GTGTCTGGCA	GTGGGCACAA	AGATGAACAA	AACAGTGCCC	CACCTTCACC	360
CCGTCAACCG	TCAGTGCAGC	AGTGGCTGG	GTGCTTGGT	CCCACAGTGA	GGAAGGCAGA	420
AGGGGTCCCT	GCCCTCAAAG	GAGGACGATA	CTCGAG			456

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GAATTCGGCC TTCATGGCCT AGCTGCCCCG CAGCACTTAC CGGAGCGACC ATGAGGGTGA      60
CGATTGGAAG CACACACAGG CTTCCCGCCA CCTCCTTTAA ACCGCCGCTG GCTTGCCAGG      120
GACAGACGGC GCGGTTGGCT CCCCAAAATT CCGACTGATA CGCGCCTCGG CGAGCGAAAG      180
CAAACGCGGG ATACTCTCGC GTTCCTGATT GGCTGCAGTT GGAATTGATC ACACCTTTTC      240
AGTTGTACTT CAATCCTGAA TTAATCTTTA AACACTTTCA AATATGGAGA TTAATCACCA      300
ACTTCTTATT TTTTGGGCCA GTTGGATTCA ATTTTTTATT TAACATGATT TTTCTATATC      360
GTTACTGTCT AATGCTAGAA GAAGGCTCTT TCCGAGGTCG GACAGCAGAC TTTGTATTTA      420
TGTTCCTTTT TGGTGGATTC TTAATGACCC TTTTGGTCT GTTGTGAGC TTAGTTTCT      480
TGGGCCAGGC CTTTACAATA ATGCTCGAG                                         509

```

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

GAATTCGGCC TTCATGGCCT AAAGCAAGTG ATTTTCTTTT TTTTAAAGAC AGGGTCTCAC      60
TTGGTCACCC AGGCTGGAGT ACAGTGACAT CATCAGGCT CACTGCAACC TTGCGCTCTT      120
GGGCTCAAGT GATTCCCCCA TCCCCACCC CCCTTCTCAC CCCCAGATTG GACTATAGGC      180
GTGTACCACC ACGCCTGGCA GAGACCGGGT TTTGCCGTTG CCCAAGCTGA TCTCGAACTC      240
CTGAGCTCAA GCGATCTGCC CGTCTCAGCC TCCCCTAAGC AAGCATTTT AAGTTTCTAT      300
GCTGTTTAAT TTTTTTTAAC TGATTAATTT ATTTGCATTG TGTGGTCATG GAATATGTTT      360
TTATGATATT GGTGTTTGA GATTGGTGA GTCTTCTTT GTAACCTAGT TAAACCATTC      420
CATATCTTTT TAAAGGATG TATATCCTT ATCTGTTAGG GCTCGAG                                         467

```

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

GAATTCGGCC TTCATGGCAG AGTGGAAGGG GTTGTAATAA TTAGGAGAGA GATAATTCTT      60
AGTGCAATTC TCTGAGGATG AAGCATGAGA TGAATCCATG GCACGAATGG AACAGCTGGG      120
GAAAGCAGGT CAGAATGGAT ATGGATATAA ATACTGTGAG TTCTCGAG                                         168

```

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

GAAGTAAATT ATTACGATTT CCTAGGTGG TTAATAAATT ACCATTATTT TCTCTATTTT      60
ACAGATCAGC AAATGATAAG TAACCTACCG AAAGTTACAT TATTTAAGTT AATCAAATGT      120
TTATTGATTG CCAGACTTTT TTCTAGGCTT AAGCAAATGT TGGAAAATAC TTCTCTGAGC      180
TTTCAAAAAT GTTATTCTA CTGTCTAGTG CTGCAGGAGT CTCTCGAG      228

```

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

GCAGAGTCAA TAGATACTTT AAATTGAAGT AAAGAATTAA AAAAGGAAGT GGATAGTTTG      60
GGTATTAGTT TAGCTAGAAA TACAAAGAAA CTTGACTTCT AGGGCAGTAC AAATTCAAGC      120
CTTCCACAAA CAAACAGTTG AGAGTATGTT TATCTTCTTA AAATGTGTGG GTGCCCTCCC      180
ACCACITTCAC CTGCTCCTCA CTGGTGCTTT GTCCCTCCC TACTACCATT CCTGTCCCGG      240
TCTCGAG      247

```

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

GGCCAAAACA AAGCTTATAA AGGTTCTGTC TCCCAACGTA ATTACCTCCA ATCGGCATTI      60
AAAGACATCC GCATTGCTTA CAGCACATCC TAGCCTCATG CTTGCCCAAG GATGGACTCG      120
AAATGAACATA TTTCCAGAGC GACTTATTCA GGCATTCTGT GGAGCCTCCG TTGCCCTGTC      180
CATCACCGGA GCTTTTGTA TGCAGCTAT GCCATTGGCC TCCGCAACC TCGAG      235

```

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAATTCGCCT TCGTGGCCTA AAAAGAAAAA ATCTAAGGTA GATTGTGCCT TTTGTGCCTT	60
TCCTCTGCTC AAGACCTTTC AGTGGCTTCC CACTTCACTC AGTAAAAGGC AAAAAGTCCT	120
TTTAATAACC TACAAGGCAT TATGTTACCC ACATTGTCCC TGCTCCCCTA CATTGTACTC	180
AAGTCTATGA TCTTTTACC ATTCTTGTA CAAAGGATT TCACTGGCTG G	231

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GAATTCGGCC TTCATGGCCT AGAAATATTT TCCTACAAGA GTACTGAATT TCAGGAAATG	60
GGATAGAGCT TCTAACCAGT GTATTCCGTC AAGTAAGATA ATAACAGCTG ACCTGCCAAC	120
AGCATTACAG GGAGATTCTT TGCTCAGCTA ACACATTCTT GTTTTCAA ATTGATGCTT	180
AATTGTAGCT GTTATTCTAA TTTGTGACAT GGAACCTAACT CATGCTTCAA TCCTTGATAG	240
AGCAAACTC AGAACAGGTT ATGTAAAAT ATAGTCTGGC TTTAGAATT GTTAATTCAC	300
CTGCTTTGCC ACAGAAATG GAGACTCGAG	330

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GAATTCTAGA CCTGCCTCGA GATCTGAACT ATAATCTTTT CCATTCTATC TAGCTCCCAT	60
CCTAAGTCCT CTCCTCCTAA CGTGGAATC TCCTAAAATC TTCTCCTTAT ACTAGGGTTC	120
GAGACATGAG GCTGTCTTTT TGGGCCTTTT GCGTTGTCAC AGTCCCAGAC CACGGAACAT	180
TCTCTCTTCC CCAGGACAGG ACATTCTCTC TTCCCAGCG CTCCCTCGAG	230

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAATTCGGCC TTCATGGCCT AAAGGGAAG TGGGAATATA CACAATGCAN AACTAGCCA	60
CATGCAATCA TGGGAGAACA GAGCTACTT AAAAATCANA CCCAAGCTTT GCTTCAGAAA	120
TAAGTGGAGT TGAACCCATT CGATCATTTA CGCATGACTT TGCAAAGGTT CTCTGGAGGG	180

GGAAGAGGAT CAACCTTCTC TCATACCGCA CAGCAAGGGA ACCAAAGTAA TATAAATCAC	240
TCTTAAAAAT GTCATGTTAC TTTAAGAATA AGCCATACTG CTGGCACCTA GAATATTTT	300
GTGGGTCCCC ATCTCTGGCT TTTCTTGTTT AAATGGCCCC CAGGCTAAGA GGCAGCTGCT	360
CACATCCCCTG CAACAAACAT GTTCTTTCCT TTCTGCATAG CCTTCCATTT CTCGAG	416

## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 289 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCGGCT TCATGGCCTA CTAGACCTGC TCAGTCGTTT CTAATGAATA AAAATCAAGT	60
GCCAAAGCTT CAGCCCCAGA TAACTATGAT TCCTCCTAGT GCACAACCAC CACGCACTCA	120
AACACCCACT CTGGGACAGA CACCTCAGCT TGGTCTCAAA ACTAATCCAC CACTTATCCA	180
GGAAAAGCCT GCCAAGACCA GCAAAAAGCC ACCACCGTCA AAGGAAGAAC TCCTTAACT	240
AACTGAACT GTTGTGACTG AATATCTAAA TAGTGGAAG TCACTCGAG	289

## (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAATTCGGCC TTCATGGCCT AATTGAGGC CTGGGTGGAA CTGACAGGTG GAGTTTGAAG	60
GCACATCTGC TAGCTCACAT AGGAAACAGA ATCTCCAGG GAAAAGACAT AGGACCTCTG	120
ACTCTAACTG AGGTTCTGGA TTATTATGAG AGATTTTCAG AAATGGTCTA ATGGTGTGG	180
CTTGCTCCAT ACCATAGATT TTAAGAGACA GTAGAGCTTC TCGATGAGA TTCCCCATA	240
AAATAATTAT GGATCTGCAC TGGCAAGCTG GTCTTGGCTC CAAAGACCAA GAGTTGGTTT	300
GTGGTGCTGA TTCTGAACCC TTGCGATGCA ACTGTCTGGT AGTAAATGG CTTTGTATGG	360
TAAGAAAGCT TTAATCCTCG AG	382

## (2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAAAAAAAC CAAACCCTAT TATTTATTG ACAGATTGTC TTAGAGTTGA TAGCATTAA	60
TAATTGAGTA AGTACAGTCC TTCCTTGTTT CCAACGTGCC CTATTTTTC TTCTTCTCT	120
ACTTTTGAT ATGCATTTTC CCTTTTCTT GTTCTTGGT GAATTCCTAA ACCTTTTCTT	180
TCAAAATCAC CTCGAG	196

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

GAATTCGGCC TTCATGGCCT AACCACATTT TTCTAATTAG TGTTCTAGAC TGGCTAGATA      60
AATCAACAAT GAATCAACAG TCTTTAAGCA CATATACAGG TATGATAACT CTGTAGTTAA      120
CTCAAATCCT TGTGCTATGT ATTATTTTGC TCGTAACTC AGAATTCAGG AAGCTACCCA      180
CCCAATCAGT CTTAGCTGT TTTATTTTCTAG TAACAAGTTT ATGCAGAACC TTCCATATCT      240
CTCATAAAAC CAGAGCATTG ATAGAACCAG AAACCTCTCGA G                               281

```

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

GAATTCGGCC TTCATGGCCT AAAAGATTG AGCATTTCAG AATTTTAAAC ATAAAAGCAT      60
AAACGTAGAT AAAATGAAGG TGTACTATGA TATCTTCAGT TTTATCAGAA ATGATGTAAA      120
AATTACAACC TCTTTAAAAA GTAGTGTTAA TCATTAGTT AGAAAAATATA TAGCTGGGCA      180
TGGTGGCAGA TGCTGTAAAT CCCAGCTACA TGGGAAGGTG AGGTGGGAGA ATCGCTTGAA      240
CCCAGGCAGT GGAGGATGCA GTGAGCCAAG ATCATGCCAC TGCACCCAG CCTGGGTGAC      300
AGAACAAGAC TCCATNTCAA GGAAGAAAAA AAAGAAAAAT ATATATATGA ACTTCAGAAT      360
CTGAGGTCAT ATATAGACAG GTCTTCCCCC CGTCCTCGAG                               400

```

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

GAAACCATAG TGGCAGATTT GTAGCAAAAA GAATCTTTGT AACCTTCCCT TTAGATGTCC      60
TGTGTTATGG CTTGGTTTTT CTCAAAGATC ATAGATTGCA GTGTTTATCT CAACTCAGTA      120
TTTCCTTTGA AAATTGAACT TTTCTCTATA TTTTCTTTC CCCCATGCAA ACTTTTTGAT      180
TGTTTTTCTG AAATCATAAT TCATTTGACT TACCAGTTAA TATTGATACA GGTCTTGCAT      240
GTTATGAAGT GCATTGTGTA CATTATCTTG TTTAATTTTC ACAACACTCT TCTCGAG       297

```

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

GGTCGCAGAA GAGTGTGAGA ACAATCAGTT AAAGAAGCTC AAAGAAATCT GTGAGAAAGA      60
AAAGAAAGAA TTAAAGAAGA AAATGGATAA AAAGAGGCAG GAGAAGATAA CAGAAGCTAA      120
ATCCAAAGAC AAAAGTCAGA TGGAAGAGGA GAAGACAGAG ATGATCCGGT CATATATCCA      180
GGAAGTGGTG CAGTATATCA AGAGGCTAGA AGAAGCGCAA AGTAAACGGC AAGAAAAACT      240
CGTAGAGAAA CACAAGGAAA TACGTCAGCA GATCCTGGAT GAAAAGCCCA AGGGGGAAGG      300
TTCCTCCTCA TTCTTGTCGG AAACCTTGCCA TGAGGATCCC TCTGTTTCCC CCAAACCTCGA      361
G

```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

GAATTCGGCC TTCATGGCCT ACTGGGGGAA GAAGGCTGCT TTATGTTTAT TTTTCAAGAC      60
TTTAAAAATA TTTTITGGTT GTATTGCACT AGGAAATCTC TCCACCTCT CCCTTTTCTC      120
TTCTTTTCCC TATACAAAT AAAAGGCCCA CCATAGAGAC TAGGCGGCCG AAAGACTAGG      180
AGGGCTGAGG AAAAGAAATA GGTCTCTGGA GGTGGAATA AACTGTGCA GCTGCCTCTT      240
CCTGGCGGTG GATGCTGCTT TGGGAGGGCC AGGGAGGCTG CAGGGGGACA GTGTTGGGAT      300
TGTCAGGAA AAAGGGGTAG GAAGGAAGGT GGAGGGATTG ATCTAGTACC AGGGAGAATA      360
TTCCACTGAA CTGTGATTCT ATGCGGCCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

GAATTCGGCC TTCATGGCCT AATTGTTTAT TGCTAGAAAA TACACAGTTT TGAGATTTT      60
GGGCATAATT GGCCTTAGTG TGTCACTTCT GCATTAAAT ATAGGTTAAT AATCAGATGA      120
AAGCAGCCAA TAACCTATGG CTTCTGTACT TTCTGGTGAA AGTTTTGTTA ATGTTTTTAA      180
TTTGATTTT TCTGCTTATA AATTGTCTT TAAATCACTC CCTCCTTCC CGCCCCCGG      240
ACTCCTTCTC CCTCCTTCCC GCCCCCCCAA CTCCTTCTCC CTCCTTCCC CGCCCGGAG      300
TCCTTCTCCC TCCTTCCCGC CCCCAGATCC TCGAG

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
GGTGACATAT TTATTGCTTC TGTTTTCCAA CTACATCACT TCAACTAGAA GTAAAGCTAT    60
GATTTTCCTG ACTTCACATA GGAGGCAAAT TTAGAGAAAG TTGTAAAGAT TTCTATGTTT    120
TGGGTTTTTT TTTCCCTTT TTTTTTTTAA GAGTATAAGG TTTACACAAT CATTCTCATA    180
ATGTGACGCA AGCCAGCAAG GCCAAAAATG CTAGAGAAAA TAACGGGATC TCGAG        235
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
GAATTCGGCC TTCATGGCCT ACCACAATCT GTTGTCTTTT CCTCTTTAGA TTCCAAAAAT    60
AACACCCCAA AGGCTACCTT TTCAAATATT CTACAACATC TGCAAAAATC TTAGTACTC    120
TGTCCTTGA GTCAAGTCAAG AAATTCCACC CCAGAAGTGT AAAAACCAAT CAATAATATA    180
TGACACTGAT TTTCTCTAAA TTATTATTTT TCTTATGGTT GAGTCTCCTG CCAACTTTAT    240
GTTTCCCAAT CGGCTCG        257
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
GAATTCGGCC TTCATGGCCT AGCTGGGCAT GGTGATGCAC GCCTGTAATT CTAGCTACTC    60
AGGTGGGGGG TTAAGGTGA GGCAAGGTCA GCGGTGAAGT GCAGCTCAGA GGGAGGGGTC    120
AAACATAAAC CAGAACTTAT AGGTCTAGAG GTAAATGGG ATTCTATGGG GGCAGAGGTC    180
AAAGGTGAAG CAGAAGTCAG GGGTGAAGGA AGGTCTGCAA AGTTAAAGGT GCGGTTTCCA    240
GAGTCAGAAG GGTGCTCGA G        261
```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAATTCGGCC TTCATGGCCT AGATTGAATT TTTAACACAG TCCTCTCAGA AACTGACTAA	60
AACAGGTTTT AAAATTAGCA AATATTAAGA ACATACGAGT AAAAGTCAGT TTATTTTAGA	120
TAAGTAGGGA TTAAATTCA AAAAAATAA ACACATTTTA AACTCCTATA ATACATTTAT	180
TTAAAATAAA TATATTTTG CCAAAAGAAG TGTAAGTTCA AAGAGTTAAC ATACAGATTA	240
TATCCTATGA GATATAATAA TATTAGAAAC TGGCTCGAG	279

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GAATTCGGCC TTCATGGCCT AGTTACATTT ATAATCAGTG AGGAAAATAT AAACATACAC	60
ATAAATGAAA GGGTCATTGG CCAATTGTTT GGAGGGAAAA AATACACCAT GTTCTAAAAT	120
AAATTTCTAG TGATTTATTG TGACTTTCAT GCATTTGGAT GATTTTAAAG ATTTTATATA	180
AAAATGAAAC CATAGCCTTA CGAGAAGAAA ATATAAGAA AACTTGTAT AGTCTTGGGA	240
GGGGGGATTG TCGAG	255

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCGATTGAAT TCTAGACCTG CCTCGAGATC GTCTTTTCTA CCTGGATGAG AGCTCTACCA	60
CTTCTTTCCT TTTGCACACT CATCTCATTG TATGCACTCT TGGGCTGTAA CTGTCATTTG	120
TTTTCCTGTA CACTCGAG	138

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAATTCGGCC TTCATGGCCT ATCATTGTC ATTAAATCTG TAGATTACAT TGAGCATTAT	60
GGACATCTTC AAAATATTTT AAATTTTGAA CAGGAGCATG CTGAAGAGTG TGTTGTTTAA	120
TTTCTATGTA TTGTACATT TTTTCTCT ATCTTATACT GCCGAGACCA GCTCAGTCGG	180
GGAGACCTTA ACCCAACGGC AGCTCGAG	208

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 268 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

GAATTCGGCC TTCATGGCCT ACATGAACT GTTAGTCACT TCATTTCTGT TTCTTCCCTG      60
TTGCAACAGC CCATCTTCGT GGAAGAACC AAGCTTTAGG CTGGGCTCTG AACAGCCACA      120
AAGTGACTTG GCTGAGGTCC TGCCATTTCC CTCATGCTCA GCAGGGGGCA GCAGACCAGG      180
GCAGTTCAGA GTATGGGGTC AAACCCAGGT CCTGTCCCC ACTCCACCTG TGGATTAC      240
CTGGATTGGG CAAGCCCCAT TACTCGAG      268

```

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCTCCCA AACCTTCAGG TAGTCAACCA      60
CCAGCAAGGC CCCACCACA GACACATCCT GAAGCTGCTG CCGTCCATGG AGGCCACTGG      120
GGGCGAGAAG TCCAGCACGC CCATCAAGGG CCCCAAGAGG GGACATCCTA GACAGAACCT      180
ACACAAGCAT TTTGACATCA ATGAGCATTG GCCCTGGATG ATTGTGCTTT TCCTGTCTGT      240
GGTGCTTGTT GTGATTGTGG TGTGCAGTAT CCGGAAAAG CTCGAG      286

```

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 199 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTATCTT AATCTCAAGA GTGTCATTAC      60
AGTGAGAATC TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA      120
CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT CTTTGTAGTC CAAGTTCAG      180
GTAGGCCATG AAGGTCGAG      199

```

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 233 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
GATTGAATTC TAGACCTGCC TCGAGTTCCA CGTCCATGGC CATCCTGAGC ATGCTGCAGG      60
ACATGAATTT CATCAACAAC TACAAAATTG ACTGCCCCGAC CCTGGCCCCG TTCTGTTTGA      120
TGGTGAAGAA GGGCTACCGG GATCCCCCCT ACCACAAC TGATGCACGCC TTTTCTGTCT      180
CCCAC TTCTG CTACCTGCTC TATAAGAACC TGGAGCTCAC CAACTACCTC GAG              233
```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
GAATTCGGCC TTCATGGCCT AAGAATAGAG AAAACGTTTT CAGCAGGCTT CACAGAGAAA      60
CCAAACAATA TTTAGAATAT GACAGCATAT GAAGAGTCTG CTACTCTCCC AGTGACCCAT      120
ACTTTCTCTT CCATCTCTGC TGGTTCTCTC TACTACCGAT TCTTTCTTGC TGTCTCTCCT      180
CTCCATCACC GTGACTTCTA TTGCCTTACT CTAATGTCTT GTCTTCTGTG TTACCCTTCT      240
GTGTGTTTTG CATTGAGAAC TCCCCCTCCG CTCGAG              276
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
GAATTCGGCC TTCATGGCCT AAAAAAAAAA AAAAATCCCT GGCTGAGAAC TATTGGATTA      60
GGGCCTCCNG TACCTATCTT TGAGGGGGAA AGGATGCTAC CATCAACTTT TCTGAATGCC      120
AGGAATGCCT TTTAGTATAG TTATTTCACT TACTATTTTA TAGCATATTT TAATTGTATA      180
GTAAGCATTG TGTCTGTTT ATGGTAAGGA AACTAAAATT GAGAGATTAG GCTGCTCGTG      240
GTGGCTTATA CCTTGTAATC CCAAGCACTC GAG              273
```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

GAATTCGGCC TTCATGGCCT AGCGAAATGA CGAAATCTAG CCCTTTGAAA ATAACATTGT      60
TTTTAGAAGA GGACAAATCC TTAAAAGTAA CATCAGACCC AAAGGTTGAG CAGAAAATTG      120
AAGTGATACG TGAAATTGAG ATGAGTGTGG ATGATGATGA TATCAATAGT TCGAAAGTAA      180
TTAATGACCT CTTCACTGAT GTCCTAGAGG AAGGTGAACT AGATATGGAG AAGAGCCAAG      240
AGGAGATGGA TCAAGCATTG GCAGAAAGCA GCGAAGGGCT CGAG                        284

```

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

GGGAACTGGA GGAAAACCAT CACAAGATGG AGTGCCAGCA AAAACTGATC AAGGAGCTGG      60
AGGGCCAGAG GGAAACCCAG AGAGTGCTT TGACCCACCT TACGCTGGAC CTAGAAGAAA      120
GGAGCCAGGA GCTGCAGGCA CAAAGCAGCC AGATCCATGA CCTGGAGAGC CACAGCACC      180
TTCCTGGCAAG AGAGCTGCAG GAGAGGGACC AGGAGGTGAA GTCTCAGCGA GAACAGATCG      240
AGGAGCTGCA GAGGCAGAAA GAGCATCTGA CTCAGGATCT CGAG                        284

```

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

GAATTCGGCC TTCATGGCCT ACTGTGTTGA CTGGTGGCT TGCTTGATAA GAAGGTTTTA      60
TGAAGCACAG CAGATATCTC AGCTGCTAAT CCTGTAAGCC CTTTACCCAT TCTCGCTTTT      120
CTCTGCTCTT GCCACATCAT GAATAGATTG GTATACTATT GTGGGATACT TCTAGTTTTA      180
GCACATGATA TAGGTTATGG TTAATGTTCC TTTCCATCTT CCTGGTTACT GATAATGTT      240
CTTTTCTGTA GATGGGTCTA TTCGATGGAA GAGTTTCAGC TTTGTTCTG TATTTCCTT      300
GGGACCTCGA G                                     311

```

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

GAATTAATCG TAAGAGAACC TCAGCATTGT GCACGATAAG AGAATGTGTC AGTATTTTCAG      60
GGTTCTACAT TTTATCTGTA AAATGTGACT TTTTITTTTT TTTATCACAA CAGAAGTAAA      120
ATGTTGCTTT GTACCTGGTG TCTTTTATTA AGAATTTACT CCCCCATT CTACAGAGA      180
ATAACAGTCG GGAGTCATTG TCACAATATA ATAGAAATGT TAGCAACCAG ATTCAATGTA      240

```

GGACTAAGTG GTCCTCATGA ATTGCATTAA GACTCTGTAC TGCTCATATT AACTCCATC 300  
CTCTCTGTAG TTTGCTGGGT ATTCTCGAG 329

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAATTCGGCC TTCATGGCCT AGAAGACAT CATTTAAGTN CTTTAAACAT TTAGTTTGTTG 60  
GTCATAAGTT GACCTTTATG TGCTTCTGA ATTGGAACTT AAAATAATCT TTAATTCATT 120  
ATTTTTTCTA CTTCTAGGCC AGTTTGTAGT TTAATATTTA TAAAAGGTGA GATAGTTATA 180  
GATAGGATTA TTTTGCAGTT TTGAAACAAC ATACAAATTG TTATAGATTT CAGAGTAGGG 240  
CTAATCACAG GAAAGACAAA AGTCAGAATG CTTNAGGTAA GCCCCTTCTC ATTATATAAG 300  
ATCAAGCTCG AG 312

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAATTCGGCC TTCATGGCCT AAAAAGTTTC AACTTAGAAA AACTAGCAAG GGATTGTTC 60  
CCCTTACCCC AGTGGTTGGT GCTAGAGAAA AAATGGAGGA TGTCTGTTCC ACGCAGACCC 120  
TGGTGGTTTA AAACACACAT ATAGATGGCT CTGGGACCAT CAAAATAGCA GCAGCAAAGA 180  
GCCACTCCAC CAGCCTCCCC TCCACTCCCC CAGGCCCCAC ACAGCAGAAG GCTCCAGCCA 240  
CTTTTGGAA GCCTGTAGCC TGGCTCCATC TTGCCCTGTG CCACAAATGC CCATGGCCCT 300  
CGAG 304

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAATTTTGAA CACTAAAGCT TTGGATACAC AAATTTATAA CATCTTATTT ATAAATCAGT 60  
GGTGTACAGA AAGCAGAGAT CCCATAATCA AGCATGGCAA ACATGTTGAA GAATATGCTT 120  
ACAATGATTT CTGCTATAGA TTTCATAATG GGGATTGAGA GAAGTAGAGT TATGGTGCTG 180  
GTTCACTGCA TTGATTGGAT CAGGCGCTGG AAAGTCTCCC TGATAGATTT TATTCTCACC 240  
TGTTGGGCAA TTTCCAGAAT ATTCTGCTGT AATTTTACAT GTGGGCTCGA G 291

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

GAATTCGGCC TTCATGGCCT AGCTAGAAAA AAAAAAAAAA AAGCCCTTTT CAGTTTGTGC      60
ACTGTGTATG GTCOGTGTAG ATTGATGCAG ATTTCTGAA ATGAAATGTT TGTTTAGACG      120
AGATCATACC GGTAAGCAG GAATGACAAA GCTTGCTTTT CTGGTATGTT CTAGGTGTAT      180
TGTGACTTTT ACTGTTATAT TAATTGCCAA TATAAGTAAA TATAGATTAT ATATGTATAG      240
TGTTTCACAA AGCTTAGACC TTTACCTTCC AGCCACCCCA CAGTGCTTGA TATTTAGAG      300
TCAGTCATTG GTTATACATG TGTAGTTCCA AAGCACATAA GCTAGAAGAA GAAATATTTC      360
TAGGAGCACT ACCATCTGTT TTCAACATGA AATGCCACAC ACATAGAACT CCAACATCTC      420
GAG                                                                    423

```

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

GCGATTGAAT TCTAGACCTG CCTCGAGCTT GGGGGGATTA CAGTTCAACA AGAGATTTCAG      60
GCAGAGACAA ATATTCCAAA CTATATCAGG AATTAAGTAG GCTTTGCTGT CCTTTGTCAG      120
CTTTGAGTCA ACCCATATGA GAGTGAATTC TCCGATCCTG TACATACTCG AG              172

```

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

GAATTCGGCC TTCATGGCCT ACCCGTGTG TCCAGTATAC CTTATAACAC TTAGCCACTT      60
CTCCCCACCC TCCAGAAGGG GTCCACGTTG AATTCTGAAT CATCTTGAAA ATAAGATTCC      120
AACCACAAAA AAAATTTAGC CATTTCTTTA CTAAAAAACA CCAAAAAACA AATCTGTTTT      180
ATAATCACAG ATTTTTAGAC AAATTTCTTG TATCAGGAAG AAATACAAAT TTTGTCATGT      240
TTCTCAAGCA GTGTCTCGAG                                              260

```

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

GAATTCGGCC TTCATGGCCT AAATAAGAT AAAAATAAAC AGATAGGAGA GCTGAATTCC      60
ATTTCAGTC CTCATGTATA TGCTTACAAA GTTCCAAATT AAGCTTGGGA CTGGTTCTTA      120
CATGGCAGGT AATCCAAACC TTTTCTATTT ACTGAAGATT TTCAGCTCTC TTACAGAAAT      180
ACACAGGCTA CCATTAAAT TGTAGGGATA AATTTTAAAT TGAATTTGAA AATAAGAGCA      240
AGTACTCGAG                                     250

```

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 260 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

GAATTGAAAC ACAGAGTTGT TCTGCTGATA GTTTTGGGGA TACGTCCATC TTTTAAAGGG      60
ATTGCTTTCA TCTAATTCTG GCAGGACCTC ACCAAAAGAT CCAGCCTCAT ACCTACATCA      120
GACAAAATAT CGCCGTTGTT CCTTCTGTAC TAAAGTATTG TGTTTTGCTT TGGAAACACC      180
CACTCACTTT GCAATAGCCG TGCAAGATGA ATGCAGATTA CACTGATCTT ATGTGTTACA      240
AAATTGGAGA AAGTCTCGAG                                     260

```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 354 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

GAATTCGGCC TTCATGGCCT AATTCATCT TTTTTCTCTG GTGCTGCATA AACATATATT      60
AAATGTTGTT ACTGATCCCT AGTACTGTTG ATTTGTGACC CTTCTCCTGA GGGAGACTAA      120
AGCTGCTTGA GCTAAAGGCT TTTGAGACAT CCCATACGGT TCCCTGAACA AAGTTTCTC      180
TCCTGACCTC AGTTCTCTTG ATGACCTTGG CAAGTGGGCC CGACTAGTTG GACACTAATG      240
AGGCATCGTA ACATGCCGGC CCCATCCTGT CCATTCTGTT CTCTTTGCCA TCTAGCATTG      300
AGTGTGTGTG CTTCTAGTG GGCATGAAGA CGGCTTTAAA ACCATCCACT CGAG          354

```

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 493 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
GCTGAAAATG CAAAACATGA AGAAAGTGAT TGAGGCAATT CGAGTGGAGC TGGTTCAGTA      60
CTGGGACCAG TGCTTTTATA GCCAGGAGCA GAGACAAGCT TTGCCCCCTT TCTGTGCTGA      120
GGACTACACA GAAAGTCTGC TCCAGCTCCA CGATGCTGAG ATTGTGCGGT TAAAAAACTA      180
CTATGAAGTT CACAAGGAAC TCTTTGAAGG TGTCCAGAAG TGGGAAGAAA CCTGGAGGCT      240
TTTCTTAGAG TTTGAGAGAA AAGCTTCAGA TCCAAATCGA TTTACAAACC GAGGAGGAAA      300
TCTTCTAAAA GAAGAAAAAC AACGAGCCAA GCTCCAGAAA ATGTTGCCCA AGCTGGAAGA      360
AGAGTTGAAG GCACGAATTG AATGTGGGA ACAGGAACAT TCAAAGGCAT TTATGGTGAA      420
TGGGCAGAAA TTCATGGAGT ATGTGGCAGA ACAATGGGAG ATGCATCGAT TGGAGAAAGA      480
GAGACTCCTC GAG                                         493
```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```
GAATTCGGCC TTCATGGCCT ACACACGGCC AAATTTGAGG GCATTCTCAC ATGTGTTCTT      60
CTCTCAAAAC CACTGGGGTT GACAGATCCA GGAGGCTAAA AAAAAGTGAC CTCTATAATT      120
CTTTAAAGGT GCTATTTTTA GAANATTGTA TAATTTATTC ACAGTATATC TAAACAGAA      180
TTAAGGACAA TTAAATATC TTATGTGACA GCCTTTATGT CTAGTCACAT TTGATGAAAT      240
AAAAAACTTC TGAATCTGAA TAGAAGTTCT ACTGTNTCAG GATTGAAGTC GAG          293
```

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
GAATTCGGCC TTCATGGCCT AAAAAGACAG GAAAATAAGT CTCTTTGTAT CCTTATTAAT      60
CATTTGAAAT TATGCTATAA TATTTTTTAA AACTCACCTG TTTGGTCTG GGTGAAGCAG      120
TTCCTGAAGG AGTGTTTGT CAGAATATAT TGTTAGGTGA ATAGAGGGTT CTGTGGCCAA      180
GTAAGTTTGG GAAATAGTGG GTTAGACAAA GTTGAGTTAC TGTTGGCCTT TCAGACCTTT      240
GATACGCTAA TGTGCATTTT AAATCTCCAA GAAGCTCGAG                                         280
```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

GAATTCTCCA GCCTGGGTGA CAGAGTAAGA CTCCATCTCA AAAACAAAAA AACCCAACAG      60
GATAAAATTT AATAGGAGTA AATATAAAGT TCTACGTTTT GATTTTAAAA ATCTAGGTAC      120
TGTATAGTGT GTATTAGTTG GGGTTCCTTT TTTGAAACTT AATCTTGCCT ATAAACACA      180
AAAGAGTTTA AGATGATATT GAGACTCCTC CTGTCCTCAT TCCTTTTCCT TCCTAATAGC      240
TCAGTCCTGA AGCTCTTAGG TGAGGCAGAA CAACTCGAG      279

```

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

GAATTCGGCC TTCATGGCCT AGGATACCTT CATTTCAAGG AGCCTCTTTA CAGTAACTGG      60
GCTAAACATT TTGTTGTCGT CCGTCGGCCT TATGTCTTCA TCTATAACAG TGACAAAGAC      120
CCTGTGGAGC GTGGAATCAT TAACCTGTCC ACAGCACAGG TGGAGTACAG TGAGGACCAG      180
CAGGCCATGG TGAAGACACC AAACACCTTT GCTGTCGCA CAAAGCACCG TGGGGTCCTT      240
TTGCAGGCCC TCAATGACAA AGACATGAAC GACTGGTGTG ATGCCTTCAA CCCACTTCTA      300
GCTCGAG      307

```

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

GAGCTGTGTC AGCATCGATC AGGGGTCTGT AGACAAAAAT TCCCAAAGAT TTGAGACTTT      60
ATTGGGGGAA ACAGATCACT GCGGGGAAT AAGCCACAGG CCAAAGGAGG AAATGCTGGG      120
ACCAGAAGTC CCGCTTGCCG CCTTTTGCTA AAAGTTCCGC ACGCCTGCTC GCGGTGGGCG      180
CAAGCATAGT GTCGTGGGG CTCTGCGACG TCTGATTGGC TCTCTGCAGT GCACCGTCGA      240
GGTAGAAGGC TCAGCTCCTA GTCGCTCCCA AATTACTTTG TTGGTGCTCG AG      292

```

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

GAATTCGGCC TTCATGGCCT AGCTTGAGGA ATGACCCAAC TCTCTCTGGA AAGTCACTTT      60

```

```

GCCTCTCTGT TCTGGTTCTC TCATTTTATA AAGTGCCTTC TTCCTTTCTG CATTTATAAG      120
TAAACATGAG AAAAATCTGA AAAGACTTCT TCAGGATGTT TAAGGAAACA AATGTTGCTT      180
TCCTTGGGTT GGGTCGTTTC ATAAGAGTGA TGTTTGCCAT AAAACTGGAG CCTCATAGAC      240
GATCTGCAG GGAGGAAGCT TTCCTTGGTC ACCTGACTCA TGTGTTTATA TATAGTATAG      300
AGGAGAGGTA TTCCAAAAGA CCCGTCGCTT TTCCTGTGTC CCACAGCTGC CTGTAGAGTT      360
GTGGCACCAT AAACTTTAGC AGCTGGAAT CCTCGAG      397

```

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

GAATTCGGCC AAAGAGGCCT ATTAATTTAA TAAAGCCATA TCATACCTCT CTTTAACATT      60
GTTAAAAGGA AACTGTGTGT GTGTATTTGT GTTAATGTTA ANTTCTCTTC ATTTTGTGTC      120
TTGGGGGGCT GTTTATTTGA GGATGTCGG GGGGCGGGTG GGTGAGACCC ATCCATCCCC      180
CATGGAAGAC CAGACCCATC CATCCCCAT GGAAGACCAT TCCCGTGTGT TCAGACTGGC      240
AGGGTACTTC CATAGACAGG AACATTCTGG ATGCTCTGAT GCTGAACACT ACCAGAATCG      300
GCCATGGATT TGCTTTGAGC AAACACCCCG CAGTCAGGAC TTACTCCTGG AAAAAGGACA      360
TCTTCTCGAG      370

```

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

GAAAAAATA GACAAACTA TGATGTAAAA ATGCTTAAAA ACAATTATTC CTCTCTGCTA      60
ATTTTAATGC AAAATAAATG ATGCTAGCAT TTAATATGTT TATATGATCT TGTTTTAGG      120
ATTGAAATTT TAATACAATG GCCTTTTGTA ACTATTTTTA CTATTATAGC TCAGGTGTTT      180
GAATTCTCTC TACCCACCT ATCACCCTA TCCCCTAACA AAGAGTCTGG CTTCAATAAT      240
ACTGTTGAAT GAAAATTGGT TCTCTAAATG GTTAACAAGA TGAATCCACA TAAATCATAA      300
TTCAGTACTG AGGAACCGAA TTTATACCCA GCGTCTCGAG      340

```

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

GAATTCGGCC TTCATGGCCT AGATTGAATT CTAGACCTGA TGTGAGAATG ATGGGCTTGG      60

```

```

AGTGTTCCTGG AAATAGCTGG GAGGCCTGTG TGTTTAGGAG CGCCTTAAAC AGTAGGATAT      120
AAGGGCAGAG AAGTAGCTGG GAACTGAGAA GAACTTTGGC TGTTATTCTA GTAAGACTGA      180
AAATTTTCAGG TGGGATTGA ACAGAGATGT GTGGTGATCT GACTTGGTTC ATTCTGCTGT      240
GGTGAAGAGA CTGGAGGTGC GGGGCAAGTA TGAAGCATG GAGACCATTA ATTTATGGGG      300
GCAATGGTAG AGGGAAGAGA AACAATGCTA TTAACGGAG TAGGAGCACA CAGAGAACAA      360
GCCACTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

GCGATTGAAT TCTAGACCTG CCTGAGATC ACCGAGTGCT TCATCTCTGA CAGTTCCTCT      60
GACCAGATGA CCACAGGCAC CAACGAGAAC GCCGACAGCA TGACATCCAT GAGCACACCC      120
TCAGAGCCTG GCATCTGCCG CTTTACCGCC TCACCACCCA AGCCCCAGGA TGGCGACCGG      180
GGCAAAAACG TGGCTGTGCC CATCCCTCAC CGGGCCAACA AGAGTGAGTG CTCAGACCAC      240
CTCCCAGGCA GTGCCCCCCC GACTCTCGAG      270

```

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

GAATTCGCCT TCATGGCCTA ATATGCTTAT GAATATGATG TTGATGGACA GCTCCAAACA      60
GTTTACCTCA ATGAAAAGAT AATGTGGCGG TACAACTACG ATCTGAATGG AAACCTCCAT      120
TTACTGAACC CAAGTAACAG TGCAGCTCTG ACACCCCTTC GCTATGACCT GCGAGACAGA      180
ATCACTCGAC TGGGTGATGT TCAATATCGG TTGGATGAAG ATGGTTTCCT ACGTCAAAGG      240
GGCACGGAAA TCTTTGAATA TAGCTCCAAG GGGCTTCTAA CTCGAG      286

```

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

GAATTCGGCC TTCATGGCCT ACTTAAATCT TAGATGCTAA TGGGAGAAAC TGATTTTTTA      60
AAAAACAGGG AACTAATTA ACATTTTATC AGATATGCTA TGAAGTAAAC AGTTGAAGAC      120
TGACAGTCCA GTGGATACCG AGGAGTTCCT TTAGATACCC TGGTGAGGTA AGGACACAGG      180
CAAGGGGAGA GCTGAGACCT GAATATGAGG AGAAGCCAGG CGAGCACACA ATAGGGCAGA      240

```

AAGGAGCAGT AGGTCAAAGC CTGAGGCAGG AGAGAGCTTG ACTGACTCGA G

291

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAATTCGGCC	TTCATGGCCT	AGAAATGGTT	CTGAAAGCGA	CAGTAGAGAG	ATGCAGTTGT	60
GATGATTTCA	ACAACCTGGA	TGTTTTCTTT	CTCCTCTTTG	CTTCCATTCA	TCTCTGTGG	120
CTGCTGTTGA	TGGAGTCAGA	CAGTAAACAC	GTGGCTTGGA	TAACACCCAT	CATCCTATGA	180
AGAATATAGG	GAGTACTTGT	TCTCTGTTGA	TTCAACTTTT	ATGTCTCCAG	TAACATTGCG	240
CTTATGAAGG	TACCTGTATT	TGTATGGACT	CTGAATAAAG	AAGAATTCAT	TTGTTTAGCA	300
AGTATTAGTT	CAGCAACCAC	TGAGAAACAA	GCACTCGAG			339

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GAATTCGGCC	TTCATGGCCT	ACATCATGTC	AAAGAGTACT	ACATACAGTT	TGGAATCTCC	60
TAAAGACCCG	GTACTACCAG	CTCGTTTCTT	CACTCAACCT	GACAAGAATT	TCAGTAACAC	120
CAAAAATTAT	CTGCCTCCTG	AAATGAAATC	ATTTTTCACT	CCTGGAAAAC	CTAAAACAAC	180
CAATGTTCTA	GGAGCTGTTA	ACAAGCCACT	TTATCAGCA	GGCAAGCAAT	CTCAGACCAA	240
ATCATCACGA	ATGGAAACTG	TAAGCAATGC	AAGCAGCAGC	TCAAATCCAA	GCTCTCCTGG	300
AAGAATAAAG	GGGAGGCTTG	ATAGTTCTGA	AATGGATCAC	AGTGAAAATG	AAGATTACAC	360
AATGTCITCA	CCTTTGCCCG	GGAAAAAAG	TGACAAGAGA	GACGACTCTG	ATCTGTAGAG	420
GTCTGAATCG	GAGCTCGAG					439

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCGAGAGGCA	GGTCTAGAAT	60
TCCAAATGTA	AAATTTACTA	AGGCTTTTCA	TGTGGAAGTA	GAATGCATAT	ATCTTTCTTG	120
ATATAACAAA	TGAATTTGGT	TGTAGCTAAC	GTGTTGTACT	AGTAAAGGTC	CACCTGCTAA	180
ACTTTTTCTT	TTTTGTTGAG	GTATAGACAG	TAGAGTGATA	CCGATACATG	AGGAAAATGA	240
GAACTGGAAT	GCAGGCCAAA	AGCTGGTCCT	TTCCAGATGA	ATGTAACCAA	GACTCGAG	298

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

GAATTCGGCC TTCATGGCCT ACACTCTCAA ATATGTGGCC TTAAACGGGA CCAAAGTAGG      60
AAAGCAGATA GTGGAAACT TCTCTCCAA TCAGACCAAG TTCACGGTGC AAAGAACGGA      120
CCCCGTGTCA CGTACCGCT TTACCCTCAG CGCCAGGACG CAGGTGGGCT CTGGGGAAGC      180
CGTCACAGAG GAGTCACCAG CACCCCGAA TGAAGCTTAC ACCAACCAACC AAGCAGACAT      240
CGCCACCAG GGTGGTTCA TTGGGCTTAT GTGCGCCATC GCCCTCCTGG TGCTGATCCT      300
GCTCATCGTC TGTTCATCA AGAGGAGTCG CGGCGCAAG TACCCAATAC TCGAG          355

```

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```

GAAAAAAGCTG GGTCAAAGAA TTACGGAAAA TGTGGGAAA TGAAATCTGT TTATGTATAG      60
TTGGTAATAA AATAGACTTG GAAAAGGAGA GACATGTTTC CATTCAAGAA GCAGAGTCGT      120
ATGCAGAATC TGTGGGAGCA AAACATTATC ATACTTCAGC CAAACAGAAC AAAGGAATTG      180
AGGAACTCTT TCTTGACCTT TGTAAGGA TGATAGAAAC AGCACAAGTG GATGAGAGAG      240
CAAAAGGCAA TGGCTCTAGT CAGCCGGGAA CTGCAAGGCG AGGTGTACAG ATTATTGATG      300
ATGAACCTCA AGCCAGACC AGTGGTGGAG GGTGCTGTTT TTCTGGATAA CTGTTACGCG      360
CTAAGAAATT AAAAGACAGA AAAAACTGT GGATCATTGC CCTCGAG          407

```

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

GAATTCGGCC TTCATGGCCT AAAAGAAAGT ACATTAAAGC AACTTGCATC TCAAAACAAT      60
ACATTCTCTT GGTGAAGTT TTAGTGAAAA TCGATTATT CCTCCTCTGA GTTTTACCCA      120
ATGGGTAAAG TTGTCTAAAT ATGGGATTCC TTAGAATCCA TCCTCCTTCC CAAGCATTTT      180
CCCATGTTTC CTTCCACCCC CAAATTCTTA CCCCATTTCA GGCAGAGCTG AGCAAAACATA      240
AGCCTTCTCT GAAGTATTGA GGGAAAGTCT GCTAAACGGC TAAACTACTT AAGGAGCTAA      300
CAGAAAAGGT TGTATCAGAG AAACAGTGA GAAACACAGG TTTCTAATTA TATCTGGCAC      360
TGGAGAGAAT GTCAAAGGTA TTGGCCAGC TCGAG          395

```

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

GAATTCTAGA AACTACAGTA GTGGGACACA TAACATAGAA GTAATCGTCC AGGATTCTGC      60
TGGAAGAAGT AAGAGTGTTT ACCACATATT TTCTGTTCAA GAGAATAATC ATCTCAGTTT      120
TGATCCCCTG GCATCATTTA TTCTCCGTAC TGATCACTAC ATCAATGGCCC GGGTCCTTTT      180
TGTGCTGATT GTGCTGAGCC AGCTCACCAT TCTCATTATT TTTAGATATC GAGGATACCC      240
AGAGCTTAAA GAACCTTCAG GGTTTATAAA TCTGACCTCA TTTTCTCTTC AATGTCTCGA      300
G

```

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

GAATTCGGCC TTCATGGCCT AAGCATGCTG TCTTGATGAT GTGATTTCAT GTGTTTCTG      60
CATGGGATTA TTAACGGCAT CCATTTTCTT GGGCGTCAAG TTGTTGCAGG TGTCCACCAT      120
TGCGATGCAG CAGCAAGAAA AACTCATCCA ACAAGAGAGG GCACTGCTAA ACTTTACAGA      180
ATGGAAGAGA AGCTGTGCCC TTCAGATGAA ATATTGCCAA GCCTTCATGC AAAACTCATT      240
AAGTTCAGCC CATAACAGCA GTCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

GAATTCGGCC TTCATGGCCT ACCCGCATCC CAGCTCTATT TAAAAAATA AAGAAGAAGA      60
TAATTCATTT CCTTAAGCTG CCCTTACACT ATTAGTCAGG AATGTTTGTG TTCACTTCCA      120
CTACATACCT TACGATCTCT TTTGCTTTCG TTTTTCCTAG TCAAGTCTCT ATTATGAGG      180
TGGACAAGCA AGATTGTCGC AAATTTTGCA CTACTGGCAT CGATGGAGCC ATGACAATTT      240
GGGATTTCAA GACCTTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC TTCATGGCCT AAACATTTTC TGAAAAACGT GATAGAAAGA AGGAGGAGCT	60
GTTTCTAGGA GGGAAATAAA TAATTGGCA GGAGACTTTT TGAAGTAGAT ATCTATTGAA	120
TAACAAAGTG ACAATGTTCC CCATCCTCTC ATTTCCATT CCAATTTTAC TTCTCGTCCC	180
AATTCAAATC ATTCTTACTT ATGATCGGCG CTATGTCAGT GCCTCTCAGC TGGTCTTCCC	240
AGACCCAGTC ACCCTCGAG	259

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 238 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCGGCC TTCATGGCCT AATTACATTT ATGCAACCAA GCTATCAAAA GGACTGGCTG	60
TCCTTGGGAA TGAAACGTAA CAAAATCGTC AATAGAGTAT TATTGGAAAA GATTGTTTTT	120
AGTCATGAAC TAGCTATTTA AATGAGAAAA CAAATGTAAT GATGCTTTCT GTCATGATTT	180
TATAAATAAA TGTCAATTGT AGGAAATTGG AAAAATAAAT GAAAAAGAAA AACTCGAG	238

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC AAAGAGGCCT ACCCTAGACC TGTTTTCTGT TCTCTACTCT TGAAATGCTA	60
ATGACCTTCA TGACCAGAGT CCGCTATTGC AGTTTGTTGGT TGACAGGCAT CTCTCACTCA	120
CTGTGCTGCA ACTCAACTCT TTATCTTTCAA CCAAACAGGG CCTCCCCGCA GCTTTCCAC	180
TGCCACTCAG TGGCACTCCA TCCAGGGTTT CCAAAGTGTA AGACCCCGGA ATTTATCTTT	240
GACACTTCCA TCTCCCTCCA CCCCTCATCC AATTCATCA	279

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 656 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

GAATTCGGCC AAAGAGGCCT AGTTATAATG ATGGAAGAAG TGGAAAAACT TTGTGATCGG      60
CTTGAAGCTGG CAAGCTTACA GTGCTTGAAT GAAACACTCA CATCATGCAC AAAAGAATAG      120
GAAAGGCTGC TTTGGAAAAA CAGATAGAAG AAATAAATGA GCAAATCAGA AAAGAGAAAG      180
AGGAAGCTGA GGCTCGTATG CGACAAGCAT CTAAGAACAC AGAGAAATCA ACTGGTGGAG      240
GTGGAAATGG AAGTAAAAAT TGGTCAGAAG ATGATCTACA ATTACTAATT AAAGCTGTGA      300
ATCTGTTCCC TGCTGGAACA AATTCAAGAT GGGAAAGTAT TGCTAATTAC ATGAACATAC      360
ATTCTTCCTC TGGAGTCAA AGAACTGCCA AAGATGTNT TGGCAAAGCA AAGAGTCTCC      420
AAAAAATTGA CCCTCATCAA ANAGATGACA TAAATATAAA GGCATTTGAT AAGTTCAANA      480
AAGAACATGG AGTGGTACCT CAAGCAGACA ACGCAACGCC TTCAGAACGA TTTGAAGGTC      540
CATATACAGA CTTACCCCT TGGACAACAG AAGAACAGAA GCTTTTGGAA CAAGNTTGA      600
AAACATACCC AGTAAATACA CCTGAAAGNT GGGAAAAAT AGCAGAAAGT CTCGAG      656

```

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```

GAATTCGGCC AAAGAGGCCT AGAGACAAAT AGGTGATACT GAATTTTATA CTGTTTTCTA      60
CTTTTCCATT AAAACATTGG CACCTCAATG ATAAAGAAAT TTAAGGTATA AAATTAAATG      120
TAAAAATTAA TTTTCAGCTTC ATTTGCTATT TCGAANCAAT CTANACTGTT GTGATGAGTG      180
TATGTCTGAA CCTGTAAATC TTAANAANACT TCCTAATCTT CTAGAAGAAA AATCTCCGAA      240
GAGCTCTCTC TAGAAGTCCA AAATGGCTAG CCATTATGCT TCTTTGAAAG GACATGATAA      300
TGGGACCAGG ATGGTTTTTT GGAGTACCAA GCAAGGGGAA TGGAGCACTT TAAGGGCGCC      360
TGTTAGTAAC ATGAATTGGA AATCTGTGTC GAGTACCTCT GATCTAAACG GTAAAACAAG      420
CTGCTGGAG AGCAGCTGTA CCTAACAATA CTGTAATGTA CATTAAACATT ACAGCCTCTC      480
AATTCAGGC AGGTGTAACA GTTCCTTTCC ACCAGATCTC GAG      523

```

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```

GAATTCGGCC AAAGAGGCCT AATTTCTTCC TGTGATATGA GAATTTCTTT TCTTTCAGCA      60
GCTTTACCTG CATTGGCTT TGGCTTTTGC AATCGGCCCC TCATTCTCGA G      111

```

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC	AAAGAGGCCT	AACCGCGGCC	GCTACTTCGG	CCTCTTTGGA	AAAAAAAAG	60
TGAAAGAAAA	NATCACAATA	CAGGGAAAAG	TGAGCTAAAA	ATCCCGGCAT	TAAAAAGCCC	120
TTGATGTGGT	CCTGAATCGG	CTATTCTAT	CTGTTCCCTG	AGCCTAACCT	CAGCGCTGGC	180
CTCTCTAAAC	CTCTTTTCAG	TCCTCTCATT	TTGAAAACAG	GGCCCATTAC	ACATTCTCTG	240
AAAGCTTGCT	GAGTGATTTA	ACCACATAGT	CTAGGGGAGG	CACTCATCAA	ACATAAGGCC	300
TCTCTTTTGG	ATTTTATCC	TATAGTGGTA	TCTATCTAGA	GGCTGGTGAA	GACAGTGTGG	360
TGGAAGGAAA	GTGGGAAGGA	TACACTGAAA	TAGGACATAG	ACGTAGAGGG	GAGTCGATGG	420
TCATCTGGCT	TGATAGGGAA	AGTTAGAGAG	CTCTCCTGAA	CCACAGTTAC	AGAGCTTGGG	480
ATTATAACAC	ACACAGCCCC	AGAGAAAACA	CTTTGTTTAC	CATATTTCCT	CTTCTGCTGG	540
GGCTCTGGCA	CCTTAATTGG	TCAAAGGCA	GCACTCGAG			579

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GAATTCTAGG	AATGGGTCGG	GAAGTTGAGA	ATCTTATATT	AGAAAATACA	CAACTGTTGG	60
AAACCAAAAA	TGCTTTGAAC	ATAGTGGAAG	ATGATTGAT	AGCAAAAGTG	GATGAACTGA	120
CCTGTGAGAA	AGATGTGCTG	CAAGGGGAAT	TGGAGGCTGT	GAAGCAAGCC	AAACTGAAAC	180
TAGAGGAAAA	GAACAGAGAA	TTGGAGGAAG	AGCTTAGGAA	AGCTCGGGCA	GAAGCTGAAG	240
ATGCAAGGCA	ACTCGAG					257

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCCTGT	AACTCGGAAA	AGATATCAGA	GGAATGTTCC	TGGCATCAGA	GAGAAAGATG	60
AGAGCTCACC	AGGTGCTCAC	CTTCCTCCTG	CTCTTTCGTG	ATCACCTCGG	TGGCCTCTGA	120
AAACGCCAGC	ACATCCCGAG	GCTGTGGGCT	GGACCTCCTC	CCTCAGTACG	TGTCCCTGTG	180
CGACCTGGAC	GCCATCTGGG	GCATTGTGGT	GGAGGCGGTG	GCCGGGGCGG	GCGCCCTGAT	240
CACACTGCTC	CTGATGCTCA	TCCTCCTGGT	GCGGCTGCCC	TTCATCAAGG	AGAAGGAGAA	300
GAAGAGCCCT	GTGGGCCTCC	ACTTTCTGTT	CCTCCTGGGG	ACCCTGGGCC	TCTTTGGGCT	360
GACGTTTGCC	TTCATCATCC	AGGAGGACGA	GACCATCTGC	TCTGTCCGCC	GGTCACTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTCTAGA CCTGCCTCGA GAAAATGAAA GTCTTTTCTC AAAAACTTC TTCCCAGGTC	60
TGTGAAGCAG CACAGTGGCC CCTTCTGGCT CTCACCTGT ACCTCGTCCT TGTTGCCTC	120
GAG	123

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCGGCC TTCATGGCCT AAGATGGCGT CTCACAAATC ATATGCCAAT TACTGAAAT	60
GGAGGTGAAA ATATTCTAGA TTTATTGTGG GATATATATA TTTATGGTG TATGGCTCCC	120
AACACCACAT GCCACTGAAC TATATAAAAC TTTATGTCAG AACACTTACT TGTGTCATAT	180
GTAACCCCTCT TGCAAATAAT ATTCCCTTAC TACAGATCTG TCCCACTGTT CTCAGAAAT	240
AAAACATGGG AACGTTGGAA TGTCTCCTTG CTATAAGATA TTGAATTCTA GACCTGCCTC	300
GAG	303

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 508 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCGGCC TTCATGGCCT ATGAAGACAA AGCTAACTTA CAAAAGCAGC TGGTTGAAGC	60
AATGAATACG CAATTAGAAC TTTCAGAACA ACTTAAATTT CAGAACAAC CTGAAGATAA	120
TGTTAAAAAA CTACRAGAAG AGATTGAGAA AATTAGGCCA GGCTTTGAGG AGCAAATTTT	180
ATATCTGCAA AAGCAATTAG ACGCTACCAC TGATGAAAAG AAGGAAACAG TTAACAAT	240
CCAAAATATC ATTGAGGCTA ATTCTCAGCA TTACCAAAAA AATATTAATA GTTTGCAGGA	300
AGAGCTTTTA CAGTTGAAAG CTATACACCA AGAAGAGGTG AAAGAGTTGA TGTGCCAGAT	360
TGAAGCATCA GCTAAGGAAC ATGAAGCAGA GATAAATAAG TTGAACGAGC TAAAGAGAA	420
CTTAGTAAAA CAATGTGAGG CAAGTGAAAA GAACATCCAG AAGAAATATG AATGTGAGTT	480
AGAAAATTTA AGGAAAGCCA CCCTCGAG	508

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 713 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```

GAATTCGGCC TTCATGGCCT AGCGGCAGTC CAGATCACGG TTA CTGTGAC CTGACTGGAG      60
AAAAATTATG TGTCTGCAAT GATAGTTGGC AAGGTCCTGA TTGTTCTTTG AATGTTCCCT      120
CTACTGAGTC TTA CTGGATT CTGCCAAACG TTAAACCTTT CAGTCCTTCT GTAGGTCGGG      180
CTTCACATAA AGCAGTTTTA CACGGGAAAT TTATGTGGGT GATTGGTGGA TATACTTTTA      240
ACTACAGTTC TTTTCAAATG GTCCTAAATT ACAATTTAGA AAGCAGTATA TGGAAATGTAG      300
GAACTCCATC AAGGGGACCT CTCAGAGAT ATGGACACTC TCTTGCTTTA TATCAGGAAA      360
ACATCTTTAT GTATGGAGGC GCCCAAGGC CCGACCCCTC CCCCAGGG GCAGTCCCCT      420
TCTTGAGGT CTCAGCTTGC GGGGTGGGGG GAGTCATGCC CAGGGGAGGA GACTTTTAT      480
CTGGAGGGGA GAGAAGGATT CTAGGGGTGT GGAGTTGGAG AAAGAGGCTT CCTTGAGCCA      540
CCCTTCCAC CCGAGCCCTT GNTGGTCCCT AGGCCAAGCC ACCAAGTGAA ACCTTCCAGG      600
ATACTAGCCC GCCAGCTGTG GGCCCCAGAA AGCCAGCTG CCTTTTAGCA CTGGATACA      660
CACAGACCA CCGAGCTCTC TGTGTTTGGC CTCTCACACA CACACAATC GAG      713

```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```

GAATTCGGCC AAAGAGGCCT AAGAGATTCA GGACCTGCAG AGTCGCCAGA AGCATGAAAT      60
TGAATCTTTG TATACTAAAC TGGGCAAGGT TCCCCCTGCT GTCATTATTC CCCAGCTGC      120
TCCTCTGTG GGGAGAAGAA GGAGACCCAC TAAAGCRAA GGCAGCAAGT CTAGTCGCAG      180
CAGCTCATTG GGCAATAAAA GCCCAGCTC TTCAGGCAAC CTGTCTGGTC AGAGTGGAAAC      240
TTCAGTCTTA CACCCCAAC AGACCTCCAC AGTCGAG      277

```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```

GAATTCGGCC TTCATGGCCT AAGGCTACCG ATATTGGAGA AGCTAACTAT GGGTTTACC      60
ACACGTAACA GCTTTTGGT GAAATCAGTT GTTATACTAA TAAGCTTTCC TCTAATTGAT      120
TTGAGTTTGG GTTTTGTGT TTGTATTGTC GGGTTTGTG TCTTTTGTG TCTTGTTTT      180
AGTAAATTGG TTTTCTTCA ATGTATTTT TAAAGTAGT CTAGCTTTAC CCAGTTTCCT      240
TGGCAAATTG AAATTTAGGC CATGAAGGCC GAATTCGGCC TTCATGGCCT ACTCAGCCTC      300
CCCAAGTAGC TGGGACTACA GCGGTGTGCC ACTATTCTCA GCTGATTTT GTATTTTATG      360
TGGAGACGGG TTTTGCCAT GTTAGTTGGC CAGGATGGTC TCTCTCTGA CGTCGTGATC      420
CGCCCGCCTC GGCCTCCCAA ATTGCTGTGA TGACAGGCGT GAGCCACCCC GCNTGGCNTG      480
TCCTACCTCT TTTTAAAGAC CTCCTCCTGT AAGCACTGGA TAATCTACTT CTAGTAATGT      540
GAAACTGACT ATATNTTGAA TTCATATGTT TTCAATCAAC CTGTTGCAGT TTATATTTCA      600
CACCTGCTC CCTTTTGACA GTTTAAGTAC AGATAGTCTC AGCAGTTCTG GAGACCATGT      660
AAAGCTCGAG      670

```

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```

GAATTCGGCC TTCATGGCCT ACGACTCTGC TCTATTTACC ACTATCAGGC CAATCCTCCT      60
GACATGCTGT TAATATTAG AAATATTTCT CCAACATTCA GAGTGCCTGG GTACCACACA      120
TGGATGCGAC TAAGATTCTT AAGTCTGGTT TCTAAGAGCT TCTTCAATGT CTCCAACATAT      180
CTTTTCAGGC TCATGTTTGA GACCTTCCTT TCAAGAATAA TTTGCTTGTG ATCTGGTTCA      240
AGCTGAACAG AGATTTTCAG ATGACTCCCA AACTATCTGC AACACATCAG CCCTATTAAC      300
TCTTCTCAGA ATGCTCATAC AGAAGCCATG CCAAGTGCACA AAAGCCACTT CTGACACCTG      360
GCCCTGTCTG ACTCATGGAT TTCTTCCAGG ATTGCTCTTT CTATCTGCTT TAAACCTCCT      420
TGCAATTGA CTTTCCTTGG CTCCAACCC ACITTTACTCG AG                          462

```

## (2) INFORMATION FOR SEQ ID NO:131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

GAATTCGGCC TTCGTGGCCT ANATATTCTA AGCATTCAAT TTGTCAAGTT CTGAGATTTT      60
CTTTCCATCT TAGTTTTTTA GAAGTCAGAA AATGACTTTT CACATTCAGT TAGGGTATAT      120
AACAAATGTTA ACGTAAGTTT ATGAGCTGAG TAGGTAGTTA ATAAACATCC TTTTAAGTTG      180
TAATGCTTTG AAATAGCATA TTAAGGGTT GCAAGGAAA ATTGGAACAT CAGTGTGAGT      240
TATTTTACAG TCATTGTAG GTCTGTTTGT GACCTTGCC TTTTCACACT TGTGTGCTA      300
TCACCTTTAG TATATTACTC TTTGGCACAG GTTGTCTAAT CACATTAATT TTTGCATCAA      360
AAATCCCTTG GTTTAGTGAT TCTTAATGAT GTTTATTTTG GAAAGTCATG GACCTGAATT      420
CTTTGAGTAG TTCATGAAAA CCATATACCT TTCCCAGAGA AATGGGGTGC ATATAATTTT      480
AGGAAGTTCA AGGTAGGGAA AACAGCTAA AAATCCCAAC TTATTTTCATC TCGAG          535

```

## (2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

GAATTCGGCC TTCATGGCCT AAGGGGATCA TCAAAGATGT TGGACACCTT GTGTTCAAAT      60
CTTGGTTTCTG GTGCGGCCCTG TGCAGATCGG CTTTGTGGTT TGGTTGTCTT GGCCTGGATA      120
CCAGTGGAGA AGATGTCATC CATATCATCA TCAAATATAG ACTTGGTTTC CACTTCTTT      180
TTGGACTTTT CTTTGTGGTT TACAGTTAAG TCAGCAAAGA TATCAATGTT ATCATCAAAT      240

```

```

AAATTAGATT CCAATGTTTT CTCCTTCTCT CTGGTTTTCT GAGAGGGTTT AATTGCTTCC 300
GTAGCAAATA TATCATCTC AAAAATATCT TGTGTTGTTA ATATGACATC CTGCTGACTA 360
CTGGATTTTG TCTCATTCTT CTGACTTC TGATCCTCGA G 401

```

## (2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

GAATTCGGCC TTCATGGCCT AGTAGATGAA CTAGAAGATG GATAAACGAA GATAGATAAA 60
ATGAAGAAAA ACAAAAGTCA AGGAGAACTC AGGCGTCCAA GAGTGTGTAA ACAACTTCTG 120
GTGTGAGACG CGCTACATTG CGCTAAATGG CCTGTGCGCT TCTGGTTTTT CCCTTCCTCT 180
GTGATTTTTT TATAGTTGTC TTTTATTTTA AACACGCCTC CCCCCCCCCT TTTTAACTG 240
ATTTTACCAT CACTCTCTCT AGCCCTGCCT CCCTAGAATT AGCTGCTTCT TACCTCCCTT 300
GGATCTGGAA CTTAAATATT AACGTGTATA TAAGTTAATA GTAAGTAGAC CGTGAATTTA 360
GAAGAGTAAA ACAGAATCAT GAGTACGTAG TCACTGTGGC CCCTTTTTTG CTGGATTTC 420
AGTTCGTAAG CATTTTTGGA AGAGAGTCGA AGGGAAGGG GTGGCTTGCC AGTCAGTTGA 480
GTGATGCATG GCTCGAG 497

```

## (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

GAATTCGGCC TTCATGGCCT AGGCTGGTCA TTGAGAGTGT TGGTGAGTC AAAGTGAAC 60
ACGATGTGAT TGGTAAACAT GTGCTTGATA CATCGAACAA AATATTCTGT CTCTGCTTCT 120
GTAAGTTGAA CAGGCTCAGA AGACTTGAAC AAGGGTCCTA TATTCAGAAA CTCAGGAATG 180
GCAGCCAATT GTTCTTGGGG ATATATTTCT AATGAAGTGC TAGACTATCC AATTACTTAA 240
TTTCTTATAC CTTTAGATAA TCAGTATGAA AAGTTCCCAT TTATAATGGA AATGAAAATT 300
CTTAACTAAA CTATACATGT AATATGTATT TCTAGAAGAG AATAAAAACC CAAGTCCTCG 360
AG 362

```

## (2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```

GAATTCGGCC TTCATGGCCT ACCCCAATCA ATGGATCCTC AACTCCAAAT CCAAAGATAG 60

```

CATCTTCTGT	CACTGCTGGA	GTGCCAGTT	CACTCTCAGA	AAAAATAGCC	GACAGCATTG	120
GAAATAACCG	GCAAAATGCA	CCATTGACTT	CCATTCAAAT	TCGTTTTATT	CAGAACATGA	180
TACAGGAAAC	GTTGGATGAC	TTTAGAGAAG	CATGCCATAG	GGACATTGTG	AATTTGCAAG	240
TGGAGATGAT	TAAACAGTTT	CATATGCAAC	TGAATGAAAT	GCATTCTTTG	CTGGAAAGAT	300
ACTCAGTGAA	TGAAGGTTTA	GTGGCTGAAA	TTGAAAGACT	ACGAGAAGAA	AACAAAAGAT	360
TATGGGCCCA	CCTCGAG					377

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC	TTCATGGCCT	AAGCAAACCT	CATGCAGCTG	GTGGAACTAG	ATGTGTCTCG	60
AAATGAGATT	CCTGAAATTC	CAGAAAGCAT	TTCATTCTGT	AAAGCACTGC	AGGTAGCTGA	120
CTTCAGCGGA	AACCCACTGA	CTAGGTTGCC	AGAAAGCTTT	CCTGAATTAC	AGAATTAAAC	180
ATGTCTTTCT	GTAATGACA	TCTCACTACA	GTCTCTACCT	GAAAATATTG	GCAATCTTTA	240
TAACCTGGCT	TCACTGGAAC	TGAGAGAGAA	TCTTCTTACA	TATCTTCCTG	ACTCTCTTAC	300
CCAGCTGCGA	AGACTAGAAG	AACCTGACTC	GAG			333

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCC	AATGAAGCCT	ACTTTAGTAT	TTTGGCACTT	CCTAATTGAC	ACCTTGGGAG	60
ACTGCAGGAA	GGGAACGAGA	ATCATTNNTA	GGNTATTGT	GTGTGTGTGT	GGTTTTTTT	120
TTTTTTTGGA	AGACAGAGTC	TCACACTTTT	GCCCAGGCTG	GAGTGCAGTG	GCGTGATCTC	180
GGCTCACTGC	AACCTCTGCC	TCCAGGGTTC	AAGCGATTCT	CTTGCCCTCAG	CTTCCCGAGT	240
AGCTGGGATT	ACAGGCACAC	GCCACAACGC	CTGGCTAATT	TTTATATTTT	TAGTAGAGAC	300
AGTCTCGAG						309

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC	AAAGAGGCCT	AAACTCAGAA	TGGTGCTACT	TGAAGACTCT	GGATCTGCTG	60
ACTTCAGAAG	ACATTTTGTC	AACCTGAGTC	CCTTCACCAT	TACTGTGGTC	TTACTTCTCA	120

```

GTGCCTGTTT TGTCACCACT TCTCTGGAG GAACAGACAA GGAGCTGAGG CTAGTGGATG 180
GTGAAAACAA GTGTAGCGGG AGAGTGAAG TGAAGTCCA GGAGGAGTGG GGAACGGTGT 240
GTAATAATGG CTGGAGCATG GAAGCGGTCT CTGTGATTG TAACCAGCTG GGATGTCCAA 300
CTGCTATCAA AGCCCCCTGA TGGGCTAATT CCAGTGCAGG TTCTGGACGC ATTTGGATGG 360
ATCATGTTTC TTGTCGTGGG AATGAGTCAG CTCCTTGGGA TTGCAAACAT GATGGATGGG 420
GAAAGCATTG TTGCAATCAC AATGAAGATG CTGGCGTGAC ATGTTCTGAT GGATCAGATC 480
TGGAGCTAAG ACTTAGAGGT GGAGGCAGCC GCTGTGCTGG GACAGTTGAG GTGGAGATTC 540
AGAGACTGTT AGGGAAGGTG TGTGACAGAG GCTGGGGACT GAAAGAAGCT GAACTCGAG 599

```

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

GAATTCGGCC TTCATGGCCT AACCTTCCTG AATATCTGCC GTTTGTCCTG CAAGAAATAA 60
CTAGTCAACC CAAAAGGCAG TATCTTTTAC TTCATTCTT GAAGGAAATT ATTAGCTCTG 120
CATCAGTGGT GGGCCTTAAA CCATATGTTG AAAACATCTG GGCCTTATTA CTAAAGCACT 180
GTGAGTGTGC AGAGGAAGGA ACCAGAAATG TTGTTGCTGA ATGTCTAGGA AAACCTCACTC 240
TAATTGATCC AGAAACTCTC CTTCCACGGC TTAAGGGGTA CTTGATATCA GGCTCATCAT 300
ATGCCCGAAG CTCAGTGGTT ACGGCTGTGA AATTTACAAT TTCTGACCAT CCACAACCTA 360
TTGATCCACT GTTAAAGAAC TGCATAGGTG ATTTCTTAAA AACTTTGGAA GACCCAGATT 420
TGAATGTGAG AAGAGTAGCC TTGGTCACAT TTAATTCAGC AGCACATAAC AAGCCATCAT 480
TAATAAGGGA TCTATTGGAT ACTGTTCTTC CACATCTTTA CAATGAAACA AAAGTCTCGA 540
G 541

```

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

CTTCATGGCC TAGTGGTTCT TCTGAAATCG GCCTTCAGAC ACCTGTCTT GGTAGTACCA 60
ATATCTAAGA AGTGGTTTCA GTTCAATTTT GTTTTCCTCC ATGCCAGAGA GAAGCCACAG 120
TTTCCTAAGC TGGGGAGGAG GTATATCCTT CAAGAGATCG GCTTGTTAGA ATAGACCACT 180
TAACACCATA TGA AAAAGCA ACAGACTGAA ACATGGATGT CCTCAAGAAG GGCTGCTGAC 240
ACCTATGATT TGGCAAGGAG ATAAATAACA GAATGTGCAA AGGGTCATAA GAGTGCAGAC 300
ACCCTAATGT CTGTTGGCTG GAAGGTCAGA GCAGTTCACC AGTGAAAATG GGTACGCCAT 360
GAAGGCCGGC CTTTCATGGC TATAGCCAT GAAGGCCGAA TTC 403

```

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

GAATTCGGCC TTCATGGCCT AGTCCTCATC TGCTGGCATT TTGTGGGGTG TTAGTGCCAA      60
ACTTGAATAG GGGCTGGGGT GCTGTCTTCC ACTGACACCC AAATCCAGAA TCCCTGGTCT      120
TGAGTCCCCA GAACTTTGCC TCTTGACTGT CCCTTCTCTT CCTACCTCCA TCCATGGAAA      180
ATTAGTTATT TTCTGATCCT TTCCCTGACC TGGTCTAGCT CCTCTCCAAA CAGCCATGCC      240
CTCCAAATGC TAGAGACCTG GGCCCTGAAC CCTGTAGACA GATGCCCTCA GAATTGGGGC      300
ATGGGAGGGG GGCTGGGGGA CCCCATGATT CAGCCACGGA CTCCAATGCC CAGCTCCTCT      360
CCCCAAACA ATCCCGACAA TCCCTTATCC CTACCCCAAC CCTTTGCGGC TCTGTACACA      420
TTTTTAAACC TGGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

GCGATTGAAT TCTAGACCTG TGTGTCTAGC TGTGATGGAA TCTGAAATGA AGTTTGACAA      60
GGACCATGAT GGACTCATTG AAAATGGAGG CTATGACAGC CAGACCTATG ATGGATGGGT      120
GACCACAGGC CCCAGTGCTT ACTGTGGAGG GCTGTGGCTG GCAGCTGTGG CTGTGATGGT      180
CCAGATGGCT GCTCTGTGTG GGGCACAGGA CATCCAGGAT AAGTTTCTT CTATCCTCAG      240
CCGGGGCCAA GAAGCCTATG AGAGACTGCT GTGGAATGGC CGCTTACTCG AG              292

```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

GAATTCGGCC TTCATGGCCT AGGGAGGCTG AGGTGGGAGG CTCACTGGAG GCCAGGAGTT      60
CGGAACCAGC CTGAGCAACA TAGGGAGACC TCAGCTCTAC AACTGAAAAA AAGATAGCCA      120
GGTGTGTTCA TGGTGGCACC TGTCTGTATT CCAGCCGCTT GGGAGGCTGA GGCAGGAGGT      180
TTGCTTGAGT CCAGGAGTTT GAGGTTGCGG TGAGCTACAC AATGAGCTAT GGTGGCACTA      240
CTACACTCCA GCCTGGGCCA TAGAGTAAGG CCCTGTCTCT AACTGGAAGT CCAAAGAGGG      300
ATCTACTTCC TAGACTATTA ATTTAATAGA TCAATAAATT AATCAAGAAT ATGATTTTTT      360
TCTCATCTTT CTCTGTAGTC ATATTTTATA CAGACTTTT GTTTAAGTAA TCTCTCTTTA      420
TGGGCAGACA ATGATTTCAG AAACACCCTG CCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

GAATTCGGCC TTCATGGCCT AGTCAGCCGT GACTGCACCA CCATACTCCA GCCTGGGTGA      60
CAGAGCGAGA TCTTGTCTTA AAACAAAACA AAACAAAACC CAGACTTCCT ATAATTCCTA      120
AAAATAAATG TGGGTTTGAG AGGCCTACCT TGAAATGTAC AAGATCCTGG CCAGACTTCA      180
CCTATCTAAC AATATGCTAG TAACTATTG TTGACATGTC TTAAAGAAAT GTTCATCAGG      240
GCCTCAGAAA GCAAGGCAGA GAACAGGTCC CTGAAATTTA CTAGCTTGCA CCAAAACCATC      300
AGATAAAGAT AGGTTAATAT TTGACAGAAA AAACCTCTCA AAAAGAGACA GTGAAATACT      360
CTTGAGATGA ATCCAGGCGG CTCTCGAG      388

```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

GAATTCGGCC TTCATGGCCT AGGCAGTGA GGCCTCTGTA ATTCTAGCAT ACAGGTGGCA      60
AGTTATTACA TTATTTCTTT CCTCCTGTCT ACCTGCAGTT GGTTTTATGT GGGGCGTTAG      120
TACACTTCCC AAAGGGCTTG CCCGAGGTG AGAGGTGCAC ATTGAACTCC CTCACCAGGC      180
AGATGGGAAG TGTGGCCATG AGAGAGAGCT TCAGGGGCCC TGGGTTTATG ACATCGCTGG      240
GCCAGGAATG AGGTTAATAT TTTAATGCG GAAGGGTGAG CCCCCTTATT ACCCGAGCTC      300
GAG      303

```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

GAATTCGGCC TTCATGGCCT ACTGGATGGC ATCTACTTCG TATGACTATT GCAGAGTGCC      60
CATGGAAGAC GGGGATAAGC GCTGTAAGCT TCTGCTGGGG ATAGGAATTC TGGTGCTCCT      120
GATCATCGTG ATTCTGGGGG TGCCCTTGAT TATCTTCACC ATCAAGGCCA ACAGCGAGGC      180
CTGCCGGGAC GGCCTTCGGG CAGTGATGGA GTGTGCAAT GTCACCCATC TCCTGCAACA      240
AGAGCTGACC GAGGCCCAGA AGGGCTTTCA GGATGTGGAG GCCCAGGCCG CCACCTGCAA      300
CCACACTGTG ATGGCCCTAA TGGCTTCCCT GGATGCAGAG AAGGCCCAAG GACAAAAGAA      360
AGTGAACAA CTCGAG      376

```

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

GAATTCGGCC TTCATGGCCT AATGGAAAGG ACAAGGAAAA GGGAGAAGGG GTGAGAGTCT      60
GTCCTAGGGG CCAACGAGAA CAGTGAGCTG TTTCAGGGGA GCCATTTCCT TGTCCATGCT      120
CACAAAGCCTG TGGATTCTTC CCCCTCTGCA GGAAATTACC TGATGTTCCA AACCCCTCC      180
AGATCCTGTA TATCCGCAGC ATCTCCCTT TCCCTGAGCT GGAACAGTTT CTACAGGACA      240
CTATCAAGAG GTACTAGGGG CCTGGAGGTT TGGGCTCCAA GAGAAGCTTG ACAGAGCCCC      300
CGCCCGACCC CTACTTCTGT TTCTTCCTAA GGTATAATCT GCAGATGTTG GAAGCTGAGG      360
GCAGCATGAA GCAGGCCCTG GGTGAAGTGC AGGCACAGCA GCCCCCTCG AG              412

```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

GCCTGGCCAT CCGGAGAGCT AAGAACCTCA GCGGCTGCT GTACGTNTCA TGCAACCCCC      60
GGGAGCCCAT GGGCAACTTT GTGGACCTCT GCAGAGCCCC ATCTAACCGG GTGAAGGGCA      120
TTCCCTTCGG GCCGTCAAG GCTGTGGCAG TGGACCTGTT CCCGCAGACC CCTTCTTTTT      180
TCATACTTAT ATGAAAGACT ACATACTTAA AATACTGGTG ATTATATTTA GGACCTGAAA      240
TCATAAGATT GTGGTCTTGC TTTTACTTAA TTTTGTATC TTAGCGATGT CTAGAGTTAA      300
TAAGTGTTGC TTTTCTAATC ACAGCAAATC TCGAG                                335

```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```

GGATTCGGCC TTCATGGCCT AGTGGGGCAC TAGGATCATC ATTTGGGTGA GAGCCCTCGG      60
CAATGGTGGA GAGGGAGAAG TTATCATTGT GGAGCTCAGA TGGGGTCCGG AATTTGTTGG      120
TCCTACGCAG CTTGGTATTC TCCGTCTTGA GCAGGTAGAG CTCTTTGGCA AAGAACACCG      180
TCATCATGAA GAGCAGGAGC AGGACGAGGG CAGCCGAGCC CACGGCCACG CACATCACCT      240
GGAAGTCGGT GATGATGGAC TCGCAGCGCA TCCCCTTGTG CCAGATGTAG TCCTGCGTGT      300
TGCACCTGCA GAAGGCCCT ATGTTCTCCA CCAGGTAGCA CTGGCCGCCA TTGTGACAGT      360
AACTTGGGAA GAGGTGCGAC ACTGACCGGC AGGAGCCGTT ATGCCGCACA AAGCCACTGC      420
GGCACTCAGT GCCATTTTCA CTGGAGGCCA AGTCCCTGCC TGGCTCTCCT TAGGCCATGA      480
AG                                482

```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

GTTCTTACT AACTTTAATG GCCACAACAT TTAGGCGAAA GGGGGGCAAT CATTGGTGGT      60
TTGGCATTCT CAGAGACTTC TGTCAGTTTC TGCTTGAAAT TTTCCCATTT TTAAGAGAAT      120
ATGGGAACAT TTCATATGAT CTCCATCACG AAGATAGTGA AGATGCTGAA GAAACATCAG      180
TTCCAGAAGC TCCGAAAATT GCTCCAATAT TTGGAAAGAA GGCCAGAGTA GTTATAACCC      240
AGAGCCCTGG GAAATACGTT CCCCCCTCT CCTCGAG                                277

```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

GCTCGCCAC TTTATGAAGA GCGATTTCAC GGCTGCTGA ACCATTGAA TTTGGATTG      60
TGTTGAGCAC TTTAAAGGT TCACTTTTT GCTTCTACCC AGATTGGTCT CAGGTCTGTC      120
TTCTCCAGAT GACCGGTGGT TTCCTGAGCT GCATCTTGGG CTGGTGCTG CCCCTGGCCT      180
ATGGCTTCCA GCCTGACCTG GTGCTGGTGG CGCTGGGGCC TGGCCATGGC CTGCAGGGCC      240
CCCACGCTGC ACTCTGGCT ACAATACTCG AG                                272

```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```

GAATTCGGCC TTCATGGCCT AGGGGCGGTG AAACGTCCTG AAGAGCGTCC AGTCGTGGC      60
CGAGAGGACT CGGGCGCTCC CCACGCTGGA GGCCGTGGAC CGTCCCTTT AAAAGTTGAA      120
ACGGCCGCCG TTCGGGACGG CCTGGCGGGA GGAGGGCCCG ACGAGGGGAG GCTTCAGGGA      180
CAACTGGGGC TTCTCGACGT CCACCCTTT CAGGGCGCGG CCCCGGTAGC CTCGGGGCCG      240
GCCCAGGTAC AGGAGGTGCT TCCCGGGACC CCCGAGTAC CTGGAGGGAC CTCCGAGGG      300
GACTCGAG                                308

```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

GAATTCGGCC TTCATGGCCT ACAATCCCAA ATGTAGGATC ATGCCCATTG CCCTAAGCCC      60
AGGCATGAGA GTCGACATCT CTCCTCTTAT ATACAGATCC AGTCCACAGG TGAAGTGGGA      120
ACTCTCCAAC CAGGATTCAG CACACCATTG ATGTTGCGAC TCCTCTACTG GAACACAGCT      180
TGGAGAAGGG ATTGGGGCTC TCATGGCAGG ATGCAATCCA CTGTTGAGAT TGTGACTCAT      240
GCAC TTGAAC CTAAGTCTCA GGAGTTGTTG ACTCTTACAC CCAGCACCCA GGTGATAGGA      300
CTCTCATGTC TGGTTCCTGC CCACAGGTGA AATTGTGACA TATACATGGT CACAGCTCAC      360
AGGTGAGGTG ATAATCACA TACCTGGATC CAGCTAAGAG AACAGATTTT GACTCTGATA      420
TCTTAGGCCA TGAAGGCC                                     438

```

## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```

GAATTCGGCT TCATGGCCTA CAAGATGACT AAAGTCTTCA CTCACCAAGG AAAAGTGGCT      60
CTGTATGGCA AGCTGGTGCA GTCAGCTCAG AATGAGAGGG AGAAACTTCA AATAAGATA      120
GATGAGATGG ATAAAATACT TAAGAAGATC GATAACTGCC TCACTGAGAT GGAAACAGAA      180
ACTAAGAATT TGGAGGATGA AGAGAAAAAC AATCCTGTGG AAGAATGGGA TTCTGAAATG      240
AGAGCTGCAG AAAAAGAATT GGAACAGCTG AAAACTGAAG AGGAGGATGC TCTCGAG      297

```

## (2) INFORMATION FOR SEQ ID NO:155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

GAATTCGGCC TTCATGGCCT AAATTTAGGA AGGTCAAACG TGAATCTCCA TTTGACAAAC      60
GTCCAACTGC AGCAGAGATT AAAGTGAAC CCACCACTGA GTCATTGGAC AAAGAGGGCA      120
AAGGTGAAAT TAGAAGCCTA GTGGAGCCAC TCAGTATGAT CCAATTTGAT GATACTGCTG      180
AGCCACAGAA AGGAAAAATA AAAGGAAAGA AACACCATAT CTCTTCAGGA ACTATCACAA      240
GCAAAGAAGA AAAAAGTGAA GAGAAGGAAG AGTTGACCAN ACAAGTCAAG TCTCATCAAC      300
TTGTTAAATC ACTCTCAAGA GTGGCTAAAG AGACTTCAGA ATCTACCAGA GTTCTAGAAA      360
GTCCAGATGG CAAAAGTGAA CAGCGTAACC TCGAG                                     395

```

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC	TTCATGGCCT	ACAGAGTACT	GAGTGGAAAC	TACGATGATA	GATTTACAAA	60
TAATGTAGCA	TACTTCTACT	TCATTGTATC	TTAAGTTTCT	TGAAATATTG	CTACTGGAGA	120
TTGGAAGAA	ATCTTAATGT	TATGGGGTAT	TGTCTAAGAA	GCTTTATTTT	AAAACCATCT	180
CATTAAATTT	TGTTGCATTT	TAGATAATCG	TCCCCAGATG	CCATGTTACC	CTAGTGCAGA	240
GTTTGGGGCT	GGATAAGTTT	TGTTGTAGG	TGGCTATCCT	GTGTTTGTGA	GGGTATTTAG	300
CAGCATCCTG	GCCTTAAAC	AAAAATGTTT	TCAGACATTG	CCAAATGTCC	CCCAGCGGT	360
AAAGTACCC	CCAAGTTGAG	AACCGCTCTA	TACAAAGAGC	TGTTATTAGA	GCCAGACTCG	420
AG						422

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAATTCGGCC	TTCATGGCCT	AGATTGCTTG	AGGCCAGAAG	TTCAAGACAG	GCTGCCCAAC	60
ATAGTGAGAC	CCCCTTCTCT	ACCAAAATTT	TAAAAATGAG	CATGCATCTG	TAGTCCTAGC	120
TATTGGGAAG	GCTGAGGCAG	GAGGATCATC	TGAGCCCAGG	AGTTTGAGGC	TGCAGTGAGC	180
TAAGAAGGTG	CCACTGCACT	GCTGTTGTCT	CTCAGCAGAT	CATTTTCAGC	TTTCTTTGGA	240
GAGTAGCCAT	TAGCAATGCA	AATGTGAAGT	TTGATAGCAC	AATAAATAAA	ACACTGAAAA	300
CTGTAGATGT	TACTTATAAA	ACACTGGCAC	TCAGATAAAT	TGGGTTTGGT	CAAGAAGACA	360
GTGAAGCATA	TCCCTGTTGG	GCCAGAGGCT	GTTATCGTTT	TGCTCTGAAT	TCAAACCTG	420
ATATGTCTCC	AAATTGCTT	AGGGTTGTTA	TCCTGGAAAA	TAGAATCTGA	TAGAAGGTGG	480
GCACATCTCG	AG					492

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC	TTCATGGCCT	ACTGCTTTG	TGAAGACAAG	ATGAAGTTCA	CAATTGTCTT	60
TGCTGGACTT	CTTGAGTCT	TTCTAGCTCC	TGCCCTAGCT	AACTATAATA	TCAACGTCAA	120
TGATGACAAC	AACAATGCTG	GAAGTGGGCA	GCAGTCAGTG	AGTGTCAACA	ATGAACACAA	180
TGTGGCCAAT	GTGACAATA	ACAACGGATG	GGACTCCTGG	AATTCCATCT	GGGATTATGG	240
AAATGGCTTT	GCTGCAACCA	GACTCTTTCA	AAAGAAGACA	TGCATTGTGC	ACAAAATGAA	300
CAAGGAAGTC	ATGCCCTCCA	TTCAATCCCT	TGATGCACTG	GTCAAGGAAA	AGAAGCTTCA	360
GGGTAAGGGA	CCAGGAGGAC	CACCTCCCAA	GGGCCTGATG	TACTCAGTCA	ACCCAAACAA	420
AGTCGATGAC	CTGAGCAAGT	TCGGAAAAAA	CATTGCAAAC	ATGTGTCGTG	GGATTCCAAC	480
ATACATGGCT	CAGGAGATGC	TCGAG				505

## (2) INFORMATION FOR SEQ ID NO:159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

GAATTCGGCC AAAGAGGCCT AGCCGGAGCA GCTGTCTGGG AGTCAAGGCT GCAGTAGCGT      60
TTCTTCATGG GGTGCTCCAG GGGGTGCCAC AGACCGACAG GCAGCCCAAG GGCCTGGACA      120
CCCCCCCCCA GGCAGGTGCT GCCCCAGGAG GACTGTCTTC GGAATGAAC CTCCCGCGGG      180
CTTTGGACTG AGGTCCCTGT GGCCTCGGTC TCCTCCCAT GAAGTGGGAG CGAGGCTCCC      240
CAATGGTGCT TTTGGCTTTA GTGTACGATG TTTGCTGTGC TTCCCGCCGT GGAGGGCAGA      300
GCCACCCAC ATCAGGATCG GACGTGCTAC CCCTCCCGGT CCCGGCCCTG GCCAGCCAG      360
CCCAGCCCTC GAG
373

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

GAATTCGGCA AAGAGGCCTA ATGAATTCTC TGATCACAAA ACAGACCCAG GAAAGCATTG      60
AGCATTTTGA GCGACAGGCA GGGCTGAGAG ATGCTGGCTA CACACCCAC AAGGGCTCA      120
CCACCGAGGA GACCAAGTAC CTTGAGTGG CCGAAGCACT CCACAACTA AAGTTACAGA      180
GTGGAGAGGT AACAAAAGAA GAGAGGCAGC CTGCATCAGC CCAGTCCACC CCAAGCACCA      240
CTCCGCACTC TTCACCTAAG CAGAGGCCCA GGGGCTGGTT CACTTCTGGT TCTTCCACAG      300
CCTTACCTGG CCCAAATCCT AGCACCATGG ACTCTGGAAG TGGGGATAAG GACGGGCTCG      360
AG
362

```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

GAATTCGGCC AAAGAGGCCT AGTTTTACAA AACGCGATTT GTAATATAAA CTAGTTAGAT      60
AACTCAGAGG GTTTTATTGG CCATATTTTT GTTTATGCTT TGTCACAGGC TTTAGTCATT      120
GCTTCCATGT GTTTTCATCC TTCAGGATAT CTTCAAGAAG CCTACTTATG GACCAAACAA      180
GTTCTGACCA TCATGGAGAA ATCTCTGGTC TTGCTCAGGG AGGTGACGGA TGGCTCCCTC      240
TATGAAGGAG TTGCGTATGG CAGCTACACC ACTAGATCAC TCTTCCAATA CATGTTTCTC      300
GTCCAGAGGC ACTTCAACAT CAACCACTTT GGCCATCCGT GGCTTAAACA ACACTTTGCA      360
TTTATGTATA GAACCATCCT GCCAGGTATA GTGAGGAGTC AGAAGTGTA AACTCGAG      419

```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GAATTCGGCC AAAGAGGCCT ACAGGTAGTA TCTTTATAGC GGTATAAAAA CAGACTAATA	60
CAAACAGGTA GCTCTAAATT GTGAGTTTTT CTTAACTCCT TTGATCTTCT GTGATAGCGA	120
TTTTTCACAT TTCACACTTC CCTAATGCCA AAAATCCACC TCCAGCAGCT GTTTTGCCTC	180
TTTCTTATCC TGCCCCCTGG AAGAATGTCA TCATTATTGC TGCCACAGCA CTGTGTTCTT	240
TTTCAGAAGT TACAGCTCGA G	261

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GAATTCGGCC AAAGAGGCCT AGTGGTCTGG GGCAAAATT AGTAAGACCT GGAAAGCATA	60
GGTAATCAAA GCAGAACTG ACAAATGAGA TGGTATCAAG CTAAAAAG	108

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 292 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GAATTCGGCC AAAGAGGCCT AGTTTAACCT CATCAGACAT TATTGCAGCC AGCTGTCAGC	60
CAAGCTCAGT AACCTTCCAA CGCTCATTTT CATGAGGCTA GAGTTCC1GA GAATCCTCTG	120
TAGCCATGAG CATTACCTCA ATCTGAACCT TTTT1TTATG AATGCTGATA CTGCTCCAAC	180
ATCTCCTTGT CCTTCCATAT CTTCCCAGAA CTCAAGCTCC TGCTCCAGCT TCCAGGACCA	240
GAAGATCGCC AGCATGTTTC ATCTGACTTC CGAGTACCGC CAGCCCCTCG AG	292

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 135 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCGGCC AAAGAGGCCT AGCAAAACT GTTCAAAAGA GTTGTGATT ACTTTTCATTT	60
CCACTTTCTC ACCCCCATTC TCCCCTCAAT TAACTCTCCT TCATCCCAT GATGCCATTA	120
TGTGGATTCC TCGAG	135

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 449 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GAATTCGGCC AAAGAGGCCT AGAAAAAGTA GCACAGTGA GTCTGAAATA GCAAGCGAAG	60
AGAAAAGCAG AGCTGCTGAG AGGAAAAGGA TTATTATTAA GATGGAGCCA GAAGATATTC	120
CTACAGATGA ACTGAAAGAC TTAAACATTA TTAAGTTAC TGATAAAGAC TGTAATGAAT	180
CCACTGACAA TGATGAATTA GAAGATGAAC CTGAAGAGCC ATTTTATAGA TACTATGTTG	240
AAGAAGATGT CAGCATAAAA AAAAGTGGTA GGAAACTCT AAAACCTCGA ATGTCAGTAA	300
GTGCTGATGA AAGAGGTGGT TTAGAGAATA TGAGGCCCC TAACAACAGC AGTCCAGTAC	360
AAGAGGATGC TGAAAATGCA TCTTGTGAGC TGTGTGGACT TACAATAACC GAGGAGGACC	420
TGTCATCTCA TTAAGTAGCC AAACCTGAG	449

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 565 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCGGCC AAAGAGGCCT AAAAGGAAAC TTGGACAAGT AGAAAGTGA TGACCCAGGC	60
TCCGTTACAT ATACTGGAT TCCAGCTGGG ACCTAGATTT GCTGAGGACG GAAGCCAAGG	120
AGACAGGAAC ATGTGGCTGC TCCCAGCTCT ACTCCTTCTC TGCCTCTCAG GCTGTTTGTC	180
TCTGAACGGC CCCGGCTCTG TGAAGTGGAC TGCGGGGGAC TCTCTGACAG TGTGGTGTCA	240
GTATGAGAGC ATGTACAAGG GATATAACAA GTACTGGTGC CGAGGACAGT ACGACACGTC	300
ATGTGAGAGC ATTGTGGAGA CCAAGGGAGA AGAGAAGGTG GAGAGGAATG GCCCGGTGTC	360
CATCAGAGAC CACCCGGAGG CTCTCGCCTT CACTGTGACC ATGCAGAACC TCAATGAAGA	420
TGATGCTGGA TCTTACTGGT GCAAAATTCA GACAGTGTGG GTCTGGATT CATGGTCACG	480
CGATCCCTCG GACCTGGTTA GGGTGTATGT TTCCCAGCA ATTACAACC CAAGGAGGAC	540
CACACATCCA GCCACCCGCG TCGAG	565

## (2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 158 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCGGCC AAAGAGGCCT AGTTTCCTTT ATATGTTTGC ACTTAATTTG ATTCCATCCT	60
TCATGCTGTT TTCATTATTC TTAGTTCATC TACACCACAT AAATTATCAC CTTTGTTTTC	120
AGTTCCCAA TTTCCATGTG CCACAAACAA ATCTCGAG	158

## (2) INFORMATION FOR SEQ ID NO:169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GAATTCGGCC AAAGAGGCCT AGTCTCACCA TCTATTCTAA ACCTTATATT ATCAATCCTA	60
TTCCCTCTCA CCAAAGAAT CCCTTTATAC AAGTAATTAT CCTGTCTATG TCTTCAACT	120
CTAGTTTCCC CACTGCAACT CTTCCTTAA TATATGTACC TGCTCTGTGA TCCCTCTCCA	180
GCTACTTCCC TATTTTCTGT TCCCCTTAC AGGAAACTT TTCTCCAGCA TTTCCCAATG	240
CCATTGTCTT ACTTCCTCAC ATTCTATTTT CTTCTCAAAC CATTTTATT AGGCTTCTTT	300
CCCCAATGGC TATTGTCAAG CTTCACTTAA TGCCGTGCAA ATCACCCTAT TCTCCAGGTC	360
TTCTTTCTTC CCAGTCTCTC GAG	383

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GAATTCGGCC AAAGAGGCCT AAATATTGTC TGAAAAAAT ATATGAGACC CATTACTCAG	60
TCTCTCTCC TGCCATTAT ACTGCAGGTA TTCCCAAGT TTCTCTCTC AACCTTTGCC	120
TCCTTTTCCC TGCTTGCTCC CTTAGTTTTC TCCTCTGGGT GGATGACTCC CAAATCTAGC	180
ACTGACCTGT TTGTCCACAT CCTTGAGTAT CCCACCACCA TTTCACACCC AGCATATCCA	240
GATGGAGCTC TTATCAGTTG TAACAGCACT GCTCAATTG AG	282

## (2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GAATTCGGCC AAAGAGGCCT AGTGAAGAG AAGAATGTTT CTGTCTCTTC CTACGTTGAC	60
TGTCTTATT CCACTGGTTT CTTAGCAGG ACTGTTCTAC TCAGCCTCTG TGAAGAAAA	120
CTTCCACAG GGCTGCACTA GCACAGCCAG CCTTTGCTTT TACAGCCTGC TCTTGCCTAT	180
TACCATACCA GTGTATGTAT TCTTCCACCT TTGGACTTGG ATGGGTATTA AACTCTTCAG	240

GCATAATTGA TGCAACTAGA GTCAATATGC TGTATATATT AATGATAGCT CTTGGGCATC 300  
GATCTCTGAA AGCTCAAATG GATGGAATTT AGTTTGCGGG AACTCTCGAG 350

## (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GAATTCGGCC AAAGAGGCCT AGGGGTGTAC ATTTTATTGG AAACCTTAAA TACTGTTTCAG 60  
AAAGAATATA TCTTCAATCA AGGCTCTTGT GCAGCCTACA CAGAAAAATG AAGCTTTTTCG 120  
GGTTAGGTGC AACGCTCGAG 140

## (2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GTGGTCTCTC CTCCCCTGCC ACTCCCCTCT TCTTTTTTTT CCAACATGGC CTTGCTCCGC 60  
GTACATCGCC ACCCAGGGAC CGCTGCCCCG CACCGTGGCT GACTTTTGGC AGATGGTGTG 120  
GGAGAGCGGC TGCCTGGTGA TCGTCATGCT GACACCCCTC GCGGAGAACG GCGTCCGGCA 180  
GTGCTACCAC TACTGGCCCG ATGAAGGCTC CAATCTCTAC CACATCTATG AGGTGAACCT 240  
GGTCTCCGAG CACATCTGGT GTGAGGACTT CCTGGTGAGG AGCTTCTATC TGAAGAACCT 300  
CGAG 304

## (2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 188 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCGATTGAAT TCTAGACCTG CCTCTCTTAT ACCTCGGTGT GGCCGAAAGG AAATAAGCAG 60  
AGGCGCTATT GGCAGGACCT AGAACTTTC CTTGTAACAT AGCTAGTATG TTCCCTCTGC 120  
CCCTTCTTCA TCTTTTCCTC ACACCTGCTG GAGCTGGAGC AGCTATCCTG ACCGCAGGTG 180  
CACTCGAG 188

## (2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 274 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GAATTCGGCC	TTCATGGCCT	ACTATCTGCC	TTGGGCTCCC	ACTGCCCTGA	CCTGTGCCCT	60
CTCACAGGCC	CCCGTGATGG	CTCGCTGGCC	TCCCTTCGGC	CTCTGCCTCC	TCCTGCTGCT	120
GCTGTCCCCA	CCGCCACTGC	CCTTGACAGG	GGCCCATCGC	TTCTCCGCAC	CTAATACCAC	180
TCTCAACCAC	TTGGCACTGG	CACCTGGCCG	AGGCACACTC	TATGTCGGCG	CAGTGAACCG	240
CCTCTTCCAG	CTCAGCCCCG	AGCTGCAGCT	CGAG			274

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GGTCAGCCGA	GCATGATAGG	AGACATCATC	AACCTCGGCC	TGAAAGGGAG	GGAGGGGAGA	60
GCAAAGTGCG	TCAACGTGGA	GATCGTGGAG	GAGCCCGTGA	GTTATGTCAG	CGGGGAGAAG	120
CCGGAGGAGT	TTCCCGTCCC	ATTCAAAGTG	GAGGAGGTGC	AAGATGTGTC	GCCAGGCCCC	180
TGGGGGTTGG	TTAAGGAGGA	GGAAGGTTAT	GGAGAAAGCG	ATGTCACATT	CTCAGTTAAT	240
CAGCATCGAA	GGACCAAGCA	GCCTCAGGAG	AACACGACTC	ACGTGGAAGA	AGTGACAGAG	300
GCAGGTGATT	CAGTGGGCGA	GCTCGAG				327

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTCGGCC	AAAGAGGCCT	AAGCAATGTC	TCCACCACTG	CTGCTGCTAC	CCTTGCTGCT	60
GCTGCTGCCT	CTGCTGAATG	TGGAGCCTGC	TGGGGCCACA	CTGATCCGGA	TCCCTCTTCG	120
TCAAGTCCAC	CCTGGACGCA	GGACCCTGAA	CTACTGAGGG	GATGGGGAAA	ACCAGCAGAG	180
CTCCCCAAGT	TGGGGGCCCC	ATCCCCTGGG	GACAAGCCTG	CCTCGGTACC	TCTCTCCAAA	240
TTCTTGGATG	CCCAGTATTT	TGGGGAAATT	GGGCTGGGAA	CGCCTCCACA	AAACTTCACT	300
GTTGCCTTTG	AACTTGGCTC	CTCCAATCTC	TGGGTCCCGT	CCAGGAGATG	CCACTTCTTC	360
AGTGTGCCCT	GCTGGTTCCA	CCACCGCTTC	AATCCCAATG	TCCTCGAG		408

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

GAATTCGGCC AAAGAGGCCT AGGAGGAATT TCCATCTTGC TCTCAAAGTG AGTCTGAATG      60
TGCTCGGTGG TGTCACCCCC GCGAGCTGC CAGTGCAGAA GGCCACTATT GAACTCCTGC      120
ACACGCCCCA ACTTGTGAGA TCGGTCAACA ACAAACAGGT TGTCTTTTTT GACTATCTTT      180
ATTGGCAGCT TGTCGAACTT ACTGGCTTGC TTGGGCTTCT CCTTTGGGTC TGCAGCGGCG      240
TCCGGGGCAG TCAGAGCGAT GCTGCTCTTT TCATCGCTTT CTGTCTTCTC GCTGTCTACC      300
TCGAG                                         305

```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

GAATTCGGCC AAAGAGGCCT AGTGCAGCAA TTTAGAGAGT GTCTCAGGAG TGTGGCTCAC      60
TGCAGCTGC AGCTATGTTA GTGCTTCTTT CTGCCTCAAG TTCAGAAACA AGCTGGACTA      120
TCTCAGGGTG ATTGAATTTT CTTGCTGTGG AATCATAGAA GTCTTGCACT CTCCAGGTT      180
TGTGTTCAAG GTCTTCATAT TCAGATGCTT GAAGAATCAT TTCACATTGG TCTAGCATTG      240
AATCGAG                                         247

```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

GAATTCGGCC AAAGAGGCCT AGTCAAGTTC ATTTCCAGA GTCTTAAGAC TAAGTTCTGC      60
CTCTCATTG CAGGTGTGCC GAGAGTTTTT TTTGAACAAC AAAAATTACT AAGGAACCTC      120
ACTACCTTTG GCGGTAGAAT TAGAAAACAG ATTCAGCAGT CACCTACTCC CCTTCAGTAA      180
TTGAGACAA TTATTTTCTT CCTGACACAA CATCAGGTCC CATGAAAAAT GACACCGTGC      240
CTGGTGT TTTT TGGGTCTTTT AATGCTTCTT TTAGAGCCAC ATTTTCTTTT TCAAACCGAG      300
TTCCCATCGC TCGAG                                         315

```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC AAAGAGGCCT AATTTTCTT CACGTTCTT ATCACCACCA TGGTTATGTT	60
GGCTGCCCTG GCTCACCATT TGTCTTACTG GGATGTTTGG TTTATATATA ATGTGTGTTT	120
AGCTAAGGTA AAAGGCTACA GGTCTCTTTC CACATCCCAA ACTTCTATG ATGCTTACAT	180
TTCTTATGAC ACCAAAGATG CCTCTGTTAC TGACTGGGTG ATAAATGAGC TGGCTACCA	240
CCTTGAAGAG AGCCGAGACA AAAACGTTCT CCTTGTCTA GAGGAGAGGG ATTGGGACCC	300
GGGATTGGCC ATCATCGACA ACCTCGAG	328

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GAATTCGGCC AAAGAGGCCT AGTTGTGGAA AAGAAAGACT GTGAGGGTAG GCACAAGAGC	60
ACTCAATGT CCCAGGTAGA GAAAACAACA TGTATGATGG CCCAGAAGGA GGCAAGTCTC	120
GAG	123

## (2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC AAAGAGGCCT ACTTGGACAA GTAGAAAGTG GATGACCCAG GCTCCGTTAC	60
ATATACTTGG ATTCCAGCTG GGACCTAGAT TTGCTGAGGA CGGAAGCCAA GGACACAGGA	120
ACATGTGGCT GCTCCAGCT CTACTCCTTC TCTGCCTCTC AGGCTGTTTG TCTCTGAAGG	180
GCCCCGGCTC TGTGACTGGC ACTGCGGGGG ACTCTCTGAC AGTGTGGTGT CAGTATGAGA	240
GCATGTACAA GGGATATAAC AAGTACTGGT GCCGAGGACA GTACGACACG TCATGTGAGA	300
GCTCACTCGA G	311

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC AAAGAGGCCT AGTTCAATCT GTAACAAGCC TTCTTCAATT TCCTCTCCAC	60
ATACCCTGCA TAGACTTTAA GATTCTCTG CTCGATGCTA ATAAGAAGAC ACACACCCCT	120

CGTTCTCGAG

130

## (2) INFORMATION FOR SEQ ID NO:185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GAATTCGGCC	AAAGAGGCCT	AGGAGGGGGA	AGAGAGTCCG	TTTTGCAGAA	GATGAAGAAA	60
AGAGTGAAAA	TTCTTCGGAG	GACGGTGACA	TAACGGATAA	GAGTCTTTGT	GGAAGTGGTG	120
AAAAGTACAT	CCCACCTCAT	GTGAGGCAAG	CTGAGGAGAC	AGTGGACTTC	AAGAAAAAGG	180
AAGAACTAGA	AAGCTGAAG	AAACATGTAA	AAGGTCTACT	TAACAGGTTG	AGTGAACCCA	240
ACATGGCTTC	CATCAGTGGG	CAGCTGGAGG	AACGTGTACAT	GGCCACACAGC	AGAAAGGACA	300
TGAATGACAC	CCTGACCTCC	GCTCTCATGG	GTGCCTGCGT	CACTGCCTCG	GCCATGCCCA	360
GCAGACTGAT	GATGGAGCAT	GTTCTCTTAG	TCAGCATCCT	TCACCACTTA	CTCGAG	416

## (2) INFORMATION FOR SEQ ID NO:186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC	AAAGAGGCCT	ACTACATTTT	TACCTAAATT	TATAGAAAAT	CAATTCGGAT	60
TGACATCCAG	CTTCGCAGCT	ACTCTGGAG	GGGCTGTTTT	AATTCCTGGA	GCTGCTCTCG	120
GTCAAATTTT	AGGTGGCTTC	CTTGTTTCAA	AATTCAGAAT	GACATGTAAA	AACACAATGA	180
AGTTTGCACT	GTTACATCT	GGAGTTGCAC	TTACGCTGAG	TTTTGTATTT	ATGTATGCCA	240
AATGTGAAAA	TGAGCCATTT	GCTGGTGTAT	CTGAATCATA	TAATGGGACT	GGAGAATTGG	300
GAAACTTGAT	AGCCCCTTGT	AATGCCAATT	GTAACGTACT	CGAG		344

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCA	AGAGCCTAAA	ATCTACAAGC	ACCAGGAAGT	CAAGATGCAA	GCACCAGCCT	60
TCAGGGACAA	GAAACAGGGG	GTCTCAGCCA	AGAATCAAGG	TGCCCATGAC	CCAGACTATG	120
AGAATATCAC	CTTGGCCTTC	AAAAATCAGG	ACCATGCAAA	GGGTGGTCAT	TCACGACCCA	180
CGAGCCAAGT	CCCAGCCAG	TGCAGGCCGC	CCTCAGACTC	CACCCAGGTC	CCCTGCTGGT	240
TGTACAGAGC	CATCCTGAGC	CTGTACATCC	TCCTGGCCCT	GGCCTTTGTC	CTCTGCATCA	300
TCCTGTCAGC	CTTCATCATG	GTGAAGAATG	CTGAGATGTC	CAAGGAGCTG	CTGGGCTTTA	360

AAAGGGAGCT TTGGAATGTC TCAAACCTCCG TACAAGCATG CGAAGAGAGA CAGAAGAGAG 420  
 GCTGGGATTC CGTTCAGCAG AGCATCACCA TGGTCAGGAG CAAGATTGAT AGATTAGAGC 480  
 GACTCGAG 488

## (2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTCGGCC AAAGAGGCCT AGGTCAGATG CATTAAAACA TATCAAAATG TTACAAAAAT 60  
 GTATGGCTCC CTGCTGAGG CCTGTGAGA TTATGTTAGA TGAGTAAACG CATCAGTGTG 120  
 TAAGTTCAGA ACCAAACGTT GAATCAAGTC ATGTACTCTC GAG 163

## (2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAATTCGGCC AAAGAGGCCT ACCTGCTCAT ACCTGTGGCC AAAAGCATGA TGCCCCAGGC 60  
 TCTGCCTCCA ATTCTACCAT CTTCTTCCAT CTTTCTCTT TATCAGGTCT CTGCCCTCCT 120  
 GTACTTTGTA CTTAGATTCT CCTCTGCCAA GCCCATTAG ACTGTGACTG GTAGGAGTGC 180  
 TGTGCTCAGC TTTCACCTG AGTGTTTATC CAAGAAGTTG GATAACCCTC TCAAGTTATG 240  
 GCCTCCATTC CAGTGGCCTC CAGTCTATGG GGATGCATTC CACTCACCTC TGGGCCTAGG 300  
 GCAGGTCGAG 310

## (2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 516 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GAATTCGGCC TTCATGGCCT AGGGCCTCAG TCTTTTFACT TTTGCGGCTG TGTTTCTCTG 60  
 AAGGCTTGGC ATTAGTAGAT TGAAAAGAAT AACCATCTAG GGAAATGTGA ATTCAAGTTT 120  
 TTTCTGACAT TCTGCTCTCT ACAAGGGGAT ATTATGTACA CATAAACCTA CTTCCAAAAT 180  
 AATGAAGTGA GGCCTAATTC CTTACTCTTC AGAGAGCCCC CTGTGGAAGT GTCACGTACC 240  
 TTGTGTATGG GCTGCCCTTC ATGGCTCTGG GAGTCATTAT AAAGGGCAGC ATTTGGCGTG 300  
 GTGCGTCCTA AGCCAGTGTT TCTCGGCTCT GTTCCTTAAA CATGTGTTAG TGTTAATAGA 360  
 TGTCTCTGGA AAAAAAAAAA AAAAAACAGC ATTCTGAGGT CAAACATGCT CAGAAAGCTT 420  
 GGAATCTGCA CTACGCTTCT CGTACACATT TCATATTAAA GATTTTGGAA AGTCCTGCAA 480

TACAGAGCCC TGTCTAATAT TGCCACAGCC CTCGAG

516

## (2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```

GAATTCGGCC TTCATGGCCT ACTTGCTAGA TAGACAGATT AAGAATGTTG AAGACATGGT      60
CCAGTTTATT AATAACATTT TGGATGGCAC AGTAGAAGCC CAAGGAGGTG ATAGCATTTT      120
GCAGAGATTG AAAAGAATAG TATTGATGC CAAATCTACT ATTGTGCTA TATTCAAGAG      180
CTCACCCTG ATGGGCTGCT TTCTCTTTGG CCTGCCACIG GGTGTCATCA GTATCATGTG      240
CTATGGAATC TACACAGCCG ACACAGATGG AGGTTATATA GAAGAACGAT ATGAAGTGTG      300
TAAAAGTGAA AATCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

GAATTCGGCC TTCATGGCCT AAGCAGAAGG ACATATTAGA GAAGGATTGT ATAGTTTCT      60
GGTAAAAGAT GACAGTGAAT TGTATGGCG ATGGATTAGC CGTGAAGGT GTTGAGTATA      120
AGTGGTCTCC AGCCAAACTC TATGGTACT GGAATAAGAG AGTAGGAACC TTCTCAGGCT      180
TTATCTTTAT CTATTCTTGT CAACAGTATG TACATGTGTC CCCCAGCCCC AAATAACTGT      240
ACAGTTTAAT GATGTTCCT CTATACAGTT CCCAGAAATC ATTGGAAATT GCTGTAACAG      300
CATATCCTCA ATGCCATCA ATTCTCCAG TCCAACCTCT CCATGGCCTC CTCTGCCTCT      360
GCTGATCTGT GAACTTCTCG AG

```

## (2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 474 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

GAATTCGGCC TTCATGGCCT AATATTTTAA AAGCGAAAGC TAACTTCTAA TTTTGAAAAAT      60
TTTTATTGGG AGCAGGATAT TATAATAATA ATCTTTAGTT GTTAAACCAT TAAACATCAA      120
GGTTTTTTAC ATTGTTTCTA TGCCTCCTCC CTCAAAAAAA AAAAACCTCC TACAATAAAA      180
CTGAAAAAAT GCACAAAGAC ATATTAGTGG AAGACCACTG CTTCGTTTAC ACAAAATGAAG      240
AGTATAAAGC AGAGAAGTGC TCCTTGGGGC AAAAGGCAAT TGGCAAAAAG CTAAGGAACA      300
TTTTCATAAT GAATTAGAAA TACAGATCAT CAGGAATATC CAGGAAGCGA TAGTGAATAC      360

```

CAGGCAGGCT TAAGAGACAG GAAACATTTA GCATGTTGGT AAACCACTTT AGCACATCAG 420  
 CAAAAGCATA TAAACAGCTT TAGGATTGGA AATTATTGCC AGGGGGGACT CGAG 474

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAATTCGGCC TTCATGGCCT ACGTNNCTAT GTCTTCAAGC ACAGAGGTGT CCAGGTGTAT 60  
 TGCACATCTT CATCGCACTG AGCTGCATGG ACAGCTGATT TCTGTGAAA AAGTATAAGG 120  
 TGATCCCTCT CAGAAAGAAA TGAAGAAAGA AAATGATGAA AAGAGTAGTT CAAGAAGTTC 180  
 TGGAGATAAA AAAAATACGA GTGATAGAAG TAGCAAGACA CAAGCCTCTG TCAAAAAAGA 240  
 AGAGAAAAGA TCGTCTGAGA AATCTGAAAA AAAAGAAAGC AAGGATACTA AGAAAATAGA 300  
 AGGTAAAGAT GAGAAGAATG ATAATGGAGC AAGTGGCCAA ACATCAGAAT CGATTAAAAA 360  
 AAGTGAAGAA AAGAAGCGAA TAAGTTCCAA GAGTCCAGGA CATATGGTAA TACTAGACCA 420  
 AACTAAAGGA GATCATTGTA GACCATCAAG AAGAGGAAGA TATGAGAAAA TTCATGGAAG 480  
 AAGTAAGCAA ATGCTCGAG 499

## (2) INFORMATION FOR SEQ ID NO:195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTCGGCC TTCATGGCCT AAGCAAAAGA GCATTAAGAA GTGTCTGTTT TTGTTATTGC 60  
 CATTTTCATA ATATTTTACT AGGTGTTCAA TTTCATTGGA TATTCCTTTT TTTTAATTGT 120  
 CTTTGTACCT ATGATTGAAA ACAGTAGTTG GTCTATGACT TTTGAGGAGA GGGAGAACCG 180  
 AAGATTACAG GAGGCCAGCA TGAGGTTGGA ACAAGAGAAT GATGACCTTG CCCATGAACT 240  
 AGTAACRAGC AAAATTGCTC TACGGAATGA CTTGGATCAG GCAGAAGACA AGGCAGATGT 300  
 GTTGAATAAA GAGCTCCTTT TGACCAAAAC CCTCGAG 337

## (2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GAATTCGGCT TCATGGCCTA AAGGAACTG ACAAAATTATC CCCAGCTGCC AGAAGAAGAA 60  
 ATCTCACTG GACGGCTTCC TGTTTCCTGT GGTTCATTAT CTGATTGGCT GCAGGGATGA 120  
 AAGTTTTTAA GTTCATAGGA CTGATGATCC TCCTCACCTC TCGGTTTTCA GCCGGTTCAG 180

GACAAAGTCC AATGACTGTG CTGTGCTCCA TAGACTGGTT CATGGTCACA GTGCACCCCT	240
TCATGCTAAA CAACGATGTG TGTGTACACT TTCATGAACT ACACTTGGGC CTGGGTTGCC	300
CCCCAAACCA TGTTCAGCCA CACGCCTACC AGTTCACCTA CCGTGTTACT GAATGTGGCA	360
TCAGGGCCAA AGCTGTCATC CTCGAG	386

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC TTCATGGCCT AGTTTTTGTG TTTTTTCTT TTTTGGTATT ATTTTGTTTG	60
CCACTTATTC CTAAAATTCA TATTGCTATT AACCGTACAC ATCTTCCAT GTTCTTATAA	120
TAATCTACAA ACATCTCTCC CTTTCTGTAG CTCTCTCTGT CACACACACA CACATGCACA	180
CACGCACACA CACACACACA CACACGCTGT GCACTCTCCT GAAGCATGTG TGTACATACA	240
TACATATGTG AGGGGTTTTA TGACTGTTT ACCAAATTGT GTTCTTAATA TATACAATGT	300
TGGCTTCTTT TTAGCCATTC AGAAGTTATT TCAGTCATGG AATGATCTCT AGCCATATAA	360
CTGAAAACAG GTAAGTTTCT TTCTTGGGGA AGAAGGGCGA ATGGTGATAG AGAAAATGGA	420
GAGCTCGAG	429

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAATTCGGCC TTCATGGCCT ACCAAGCTAT GCAGGAACAG TTGTCTAAGA ACAAAGAACT	60
GACACAGAAA CTCAGGTAG CCTCTGAGAG TGAGGAAGAG GAGGGAGGCA CAGAAGATGT	120
GGAAGAACTC CTTGTCCCTG ATGTAGTGAA TGAAGTGCAG ATGAATGCAG ATGGGCCGAA	180
TCCTTGATG CTCAGGAGCT GCACCACTGA CACCAAAGAG GCTGCAACCC AGGAGGACCC	240
TGAGCAACTG CCAGAGCTTG AGGCCCATGG AGTTTCTGAA AGTGAGGGAG AAGAAAGACC	300
AGTGGCAGAA GAAGAAATTT TGTTGAGAGA ATTTGAAGAA AGGCTCGAG	349

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTCGGCC TTCATGGCCT AGGGAAAGCT CCAACTTGCT TTACCTTTCT AAGATATCCC	60
ATTTTCTCTA TACCATTGTG TGACTAATAT ATCTCTTGCC CACTGGTTTG TAACAGTGCC	120

TTAATTAGTT TTTGTGTTTG AAGTTCCAGA ATCTCTTCCT GGCCTATGTA TTGTGTTCCG	180
TTGATGGATC TTTCCATCCC ATGGTACCCT TTAATAATTAT TGTCTTCATT TTTATTACTA	240
TTGTTATGCC CTTTCTCTC TCCGTGCACA TCTTCATGTT TGAACCTAA AAACACACCG	300
CCAACGCTCG AG	312

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GAATTCGGCC TTCATGGCCT AATATATCCA AGTAATAGCA TGTACAGTTT GGTAAGCAAT	60
ATAATAGAGA GATATTCACA GTGAAATAGG AAAGAGCAGT ATAGGTGCAA AGACAAAAAG	120
CATGACACAG CTAGATACAG GGCAGCTGTT ATTGGTTTGG TATGGAGAAA ACCTGGAGAA	180
ATGGTGAGAG AAGGGGCAGA AGATGAGAGG GGCCAGATCA TGGAGTACCT GTTTGTGGCG	240
CTCAGGAGTT TAGATGTTAT CATGCAGATA ACTAGGAGCC ATTGAGGAA CTTAAATACA	300
GGAGTGATAC CAGATTATA TGTTTTAAA ATGATTACTT GGTGTAATT AAAGAAAAGA	360
TTGGATGATT TAGGCAGATC TCGAG	385

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

AATTCGGCCT TCATGGCCTA CGTTTTTTTA AATTTTTTTA ACTACATATT TGATACGATC	60
TTTTCTTCT TGCCTTCTTT TTGATTACTT ACTTTCTACC ATTCTATGTT TTTCGTCCT	120
AGTTTGAAAA TTGTATACTT TGTTTTATT CTTCAGTGG TTACCCTAGA AATTACAACA	180
AACAAAAATT GCAACAACCT CGAG	204

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GAATTCGGCC TTCATGGCCT AAAATCATCA TGCATATTTA TTTCTCCAAA GCACCTTTGA	60
CAAGCATGAT TTGGATAGAG ACTGTGCTTT GTCACCTGAT GAGCTTAAAG ATTTATTTAA	120
AGTTTCCCT TACATACCTT GGGGGCCAGA TGTGAATAAC ACAGTTTGTA CCAATGAAAG	180
AGGCTGGATA ACCTACCAGG GATTCTTTC CCAGTGGACG CTCACGACTT ATTTAGATGT	240
ACAGCGGTGC CTGGAATATT TGGGCTATCT AGGCTATTCA ATATTGACTG AGCAAGAGTC	300

TCAAGCTTCA GCTGTTACAG TGACAAGAGA TAAAAAGATA GACCTGCAGA AAAAACAAAC	360
TCAAAGAAAT GTGTTTCAGAT GTAATGTAAT TGGAGTGAAA AACTCTGGGA AAAGTGGAGT	420
TCTTCAGGCT CTCTTGGAG AAGACTCGAG	450

## (2) INFORMATION FOR SEQ ID NO:203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GAATTCGGCC TTCATGGCCT AACTGGTTTC TGGCTCGTGG ANTCTGTTTC AAGATCATAT	60
AAGCCGTTGC CATTCCCAAG NAGCGCTGGG ATATGCTCCT TCTCAGATGC TGCTATTTCA	120
GTGAAGGTAT TTAATGCTTG TTCAACATTA GATTTCGTGT TGGTAGCCAT TAAGCAATAG	180
TTTTCCATTA TGCGAANCTG TACGTGACCC TGAACAGTCT GAGGTTTTCAG TTCCTTAANA	240
AGTTTTCTG CTGTTCTTAC TGCCAGTTGC ACAGATTCTT GCTTCTCAGT TGAATAACCC	300
AGGTCTCCAT CCAGGTTTTC AAATACTTCA CCTCCAACAG TTTCATTATC TGGATTCAAA	360
CAGATCTCTA TCATATTATA AAGGGCATTT TGGCCCCAGT CACGATCTTT CCGAGCTTTA	420
TTAAATGTC GAAGGGCATC ATTTGTTCTT CCAGTGATAC AAAGATACAG TCCTTTACAA	480
TACTGAAATC CTGGTTCCAA TTTTGCTCTG GAGNNACGTT TCTCAGCCAT TGAGAAAAAT	540
CTTGGGACAT CCCTCGAG	558

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GAATTCGGCC TTCATGGCCT ACAAGTAGGG ACTGACTTCT CTAGGTTTCCT ACAAAGCTCT	60
TCAACCACAC TCATTTCAAG CTCTGTCAGA ACAGCATCTG AATTAGGAGG ACTTTGGGAT	120
TCTGGGATAC AGGAAGTATC CAGAGCTTTG GATATAAAAA ACCCTGGGAC AGATATTTTG	180
CAGCCTGAAG AGACCTATAT AGACCCTACT ATGATACAAT CTTTAACTTT TCCTTTGGCC	240
CTTCATAATC AAAGCTCGA TAAGACAGCT AACATTGTGG AAAACCCATG TCCTGAGATT	300
CTAGGAGTGG ATGTAATATC TAAAGAGACA ACTAGGAGGA AGCTCGAG	348

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GAATTCGGCC TTCATGGCCT AAGAAAAAAA AGAAAGAAAA AAAATGATAC TTTCCAGGTT	60
---	----

CGCTTGGGTC CAGATCTGTA TTCCCAGGGC TCATAGAGAT ATTGGCAAAC TGACAGATT	120
CATGGCTCAA GAAACCTAAA GACACCTACT TGAATTCCTT TGGTTGGCAG TCAAATGTTA	180
ACTAGTGTGT TTTCAAGCTT CTATTCTTAG GCATGTTACT TCCTTTTGA AGTCAAAACC	240
AACCATCTTT TAAGTAAGAG GGCTAACCA ATATGTGCCA CACTAACTCG AG	292

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTCGGCC TTCATGGCCT AAAATATTAA AATCTTTGAA GAAGAAGAAG TTGAATTTAT	60
CAGTGTGCCT GTCCCAGAGT TTGCAGATAG TGATCCTGCC AACATTGTTT ATGACTTTAA	120
CAAGAAACTT ACAGCCTATT TAGATCTTAA CCTGGATAAG TGCTATGTGA TCCCTCTGAA	180
CACCTCCATT GTTATGCCAC CCATCTCGAG GCAGGTCTAG	220

## (2) INFORMATION FOR SEQ ID NO:207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GAAAAAATGG CCAAGGCTAC TGGGAACTA AAGCCAACTT CTAAAGATCA GGTATTGGCC	60
ATGCTAGAGA AAGCCAAAGT TAACATGCCA GCCAAGCCTG CTCCACCCAC TAAAGCAACT	120
TCTAAACCAA TGGGAGGGTC CGCTCCAGCC AAATCCAGC CTGCATCAGC ACCTGCTGAA	180
GATTGTATTT CCAGCAGTAC AGAACCCTAAA CCTGATCCAA AAAAGGCCAA AGCTCCAGGA	240
TTATCCTCTA AAGCAAAGAG TGCACAAGGG AAGAAGATGC CAAGCAAAAC CAGCTTAAAG	300
GAGGATGAAG ACAATCCGG GCCTATACTC GAG	333

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GGAGACAAGT TCTCCTCAGT GAACTGGCAG TACCAGTGTG GGCTTACCTG TGAGCACAAG	60
GCCGACCTTC TCCCTATCAG TGCATCCGTC CAGTTTATTA AAATTCCTGC ACAGTTACCC	120
CACCCCTGTA CAAGATTCCA GATCAATTAT ACAGAGTATG ACTGCAACAG AAATGAGGTG	180
TGTTGGCCGC AGCTTCTATA TCCATGGACT CAGTATTATC AAGGGGAGCT GCATTCTCAG	240
TGTGTTGCTA AGGGCTTACT GTTGCTGTTG TTCCTCACAT TGGCCTTGTT CCTCAGCAAC	300
CCCCGGACCA CTCGAG	316

## (2) INFORMATION FOR SEQ ID NO:209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

GAATTCGGCC AAAGAGGCCT ATGTCCTGT CCATCTAGA GGCTGACCAA GCCCAGCCAT    60
GGGTGGTCCA AATTGCTTAG GTGGTCCCAA TTGCTTGGCT GGCCCAAGAG ATGTCTGGTT    120
CTTAACAATA CAAGAGCCTA TAGAAATTGC TAAAGGGATT TCAGCCACAA CTGAAGCTCA    180
CCAAGAATGA GTTTTCTGGA ACTGGTAAA GTGTCACAGT AGGGAGTAAG GAAATAAGAA    240
TCCCCACCAA ACATAAGAGA ACAGAATGAT AATAGTCCCT ACTAGTCCAT GACAAGGCTG    300
CCAATTAGGC ATTAAAGCT ATCAAAGATG ATGCTGTGAG GGACCTGGCA ACTTTTGTA    360
TAGTCTGACT TTAATGTTT TATTAATGGC CAAGCAGCAA ATATTTTAGG ATTTGTAGGC    420
TATATGGTCT CTGTCCCAAT TACTCCATTC TGCTACTGTA GCATAAAAGC AGCGATACAT    480
CCTAAACCCG TCGATTGAAT TCTAGACCTG CCTCGAG    517

```

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

GAATTCGGCC AAAGAGGCCT AAGAACATGA AACATCTGTG GTTCTTCCTT CTCCTGGTGG    60
CAGCTCCCCG ATGGGTCTCTG TCCCAGGTGC AGCTGCAGGA GTCGGGCCCCA GGACTGGTGA    120
AGCCTTCGGA GACCCTGTCC CTCACCTGCA CTGTCTCTGG TGATTCCATC AGTCATTACT    180
ACTGGACCTG GATCCGGCAG CCCCCAGGGC AGGGACTGGA GTGGATTGGA TATTTCTATT    240
CACCCGGGAA CTCCAACTAC AATCCCTCCC TCAAGAGTCG AGTCACCATG TCAGTCGACA    300
CGTCCACGAA CCAGTTCCTC CTAAAACTCA NTCTGTGAC CACTGCGGAC ACGGCCGTCT    360
ATTACTGTGC GAGAGACCTA TATTGCCGTG GGGGAACCTG CTACCCCGCG AGACTTGACC    420
GCTGGGGCCA GGGAAACCGG GTCATCGTCT CGTCAGCCTC CACCAAGGGC CCATCGGTCT    480
TCCCCCTGGC ACCCTCTCTC AAGAGCACCT CTGGGGCACA GCGGCCCTGG GCTGCCTGGT    540
CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAT TCAGGCGCCC TGACCAGCGG    600
CGTGACACAC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT    660
GACCGTGCCC TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC    720
CAGCAACACC AAGGTGGACA AGAAAGTTGA GCCCAAATCT TGTGACAAAA CTCACACATG    780
CCCACCGTGC CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTC    829

```

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GAATTCGGCC AAAGAGGCCT AGTTAATCTG ATAAATTCAC CATCAATTG GTAAGCTTTA	60
ATATAACTAC CTGTTTTTTT GAATACAGAT AATGCAAAAG AAAACCATT TATACTCGGC	120
TATATACCTT CCACCACTCG AG	142

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GAAATTCGGC CAAAGAGGCC TAGTGAATC ATTCTGCCAC ACCATTTCTT ACTCAAATAG	60
GTACAAACAT ACCACAGACA CTCCCATATA CACATGCTCC TCTATCCGCC AACTCTGGAA	120
CCAAAACATA ATTGGTCTTC AAGAGAGATG ATGGCTTTAA GAACAAAAAT AGCCTTATCC	180
TCTATTTTAC TTGCTGTACT GTTGTACTGT TTATTTAAGA AACAAAGCTGG TGGTTGATGT	240
CCAGGAAAAA TTATCTTTTC AAAATGAGGG AAGAGGAGGT TCACCATGTG GATATGGTGT	300
GCCTTTCAAC ATCCTTAAGG ATTGTTGATA TCATTATTGT TAATCAATTG TTGTCAGCAC	360
AGTGGCTGCC CAAGCTGTGC AAATGAAACA GCCAATCAGC AGGAGAAAGT GATGAAATTA	420
AATGACCTCT TTCCTTAACC ACTCATCCGT AAGCCTTGTT ATTTTTCATA CAAACCTCGA	480
GCCGGGGGAG GAGGGGCGGC GGCGAATGCT GGGAGAGTCA GGTCTAGAAT TCAATCGTAG	540
GCCTCTTTGG CCGAA	555

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAATTCGGCC AAAGAGGCCT ACGAGAAGGG CGGTGTGTAC AAAGGGCAGG GACTTAATCA	60
ACGCAAGCTT ATGACCCGCA CTTACTGGGA ATTCCTC	97

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GAATTCGGCC AAAGAGGCCT AAGAAGAAAT TGGTAGATTG CGAGAAGAGA TAGAAGAATT	60
AAAAACGTAAT CAGGAACCTT TACAAAGCCA GCTGACTGAA AAGGACTCTA TGATTGAAAA	120
TATGAAATCT TCCCAAACAT CTGGCACAAA TGAACAGTCT TCAGCAATAG TTTCAGCTAG	180
AGATTCTGAA CAAGTTGCAG AATTAAAACA GGAAGTGGCA ACTTTAAAGT CTCAGTTAAA	240

CTCACAATCT GTGGAGATCA CCAAACTACA GACAGAAAAG CAGGAACTGT TACAGAAAAC	300
AGAAGCGTTT GCAAAATCAG TTGAGGTACA AGGAGAGACC GAGACTATAA TAGCCACCAA	360
AACTACTGAT GTAGAAGGAA GACTGTCAGC ATTATTACAA GAGACCAAAG AGTTAAAGAA	420
TGAAATTAAA GCTCTGTCTG AGGAAAGAAC TGCCATTAAA GAGCAGCTGG ATTCATCTAA	480
TAGTACC	487

## (2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 584 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GAATTCGGCC AAAGAGGCCT ACTGGGCCTT TCAGCACCTG CTCCAGCTTC ACCTTGGTGA	60
ACATCAGGTT GAAGTTCTCA GGGTGCTCGG TGATGGCCAT GTTGACAACA TCCAGGGCAT	120
GCTGGTGGTG CTTCTGGGCA GAGAAGAGCA GTGCCAGCAG GTGGAGGGCG TGGGCATCAT	180
CCTTGCCTAC CTTCAGGGCC TCCTGCAGCT GCTCCATGGC ACTGGAGATC TGTCGGACGA	240
GGGCCAGCTG CAGCGAGACA TAGAGGATGA CCTGGGGGTC ACTGGGCGCC AGCTGCTGAG	300
CCCTCTCCAG CGTCTGCAGT GCCTTCCGGT GCAATTCATC TTGCTTGGAC TTCAGGGTGG	360
CGTCGGTGGC CTGCAGGCTA TAGGTGAGAC CCAGAGCCAG GTAGCCCTTG GGGAGGAACT	420
CCCCGGCTTC CTCTCCGAGG CTGATCACCA TCATGGCAAA GTGCTCTGCT TCCTCTAGCC	480
AGCGAAGGGA CCCGATGCAG ACCTTCGCGG CATCAGGGG CACGGTGGGG TCCGAGGGCC	540
GCAACTTCAC ACACTCCCGC AGCAGGGACA CAGCGTAGGC TGAC	584

## (2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 532 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC AAAGAGGCCT AGACCTGCCC TAAAGATAGA GTCTTGATGC ACCGTCTACC	60
TTGTCCCCAA CCAAGAGTGA GTAGTGCACA GAAGTCTCCT GGCACCTGGA GAATCCTGCA	120
TTTTTAATGG ACGAGCAGGG CAGGAAAGAA AAAAAAACC CAAACCCCAT CACTCTGCCA	180
GCCCCTGTGA CCAAAGCAGC CCAAATCAGT TACCTTGACA ACTCTCATGC ACAGACTGCA	240
CCAGCCTGTG TTGCAAACAT CACTGCCCCG CTTCTAACAG GAAGAGATAC TCTTTTGGGG	300
GTCTTGCAGG GCCCAGGACC AGAGCCCCCT CTACCCAGGG CCCTTCCAAA GGCAAAGCAC	360
AGAGTCACAT TTGGGCGTGG CATGAGAGGG AAATAAAGAG ATTTGGCTGT AGTGGGAGGG	420
AGGTTTCAGT GCTTTTCTG GGGACATTGG TGCCTATCTC TATTCTGAGA GTTGTCTCC	480
TCATAGGACA CCATAAATCG CATCCAGGAC CTGCTGGCTG AGGGTACTCG AG	532

## (2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC AAAGAGGCCT AGTGTGTCCG GGTCTTATAC AAAACAACA CAGTGAATGA	60
AGGAATAAAT ATTTATTGAA TGGAAAATCA GCAAAGGAAA AAATTGTATA ATTGTCAATG	120
ACAATGGGAA GCACATAGTG AGGCTATGAG TGATTTGGAA ATCATGAGCG TGCAGTGTTC	180
TGTTACGCA TTTCGGTTGT GTTTTCAGAA AGTAACTACA ACATAGCATC ATGTAGCAGA	240
ATTGCTGGTT GTAAGCAAAA AGGCTCGAG	269

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC AAAGAGGCCT AATTCTTTT CTTTTTAATT TGAAGAAAA TCATCAGTCT	60
TGGAATACAG AAGAGAAACT AGAAATATAC GTATTTTGT TCACATTTGA ACAGTCATTC	120
TTGAGGAATA CTCCATACCT GAGTAGACAG CCATGTGGCC ATCGCAGCTA CTAATTTTCA	180
TGATGCTCTT AGCTCCAATA ATTCATGCTT TCAGCCGTGC CCCAATTCCA ATGGCTGTGG	240
TCCGCAGAGA GCTATCCTGT GAGAGCTATC CTATAGAGCT TCGCTGTCCA GGAACAGACG	300
TCATCATGAT AGAAAGTGCC AACTATGGCA GGACTGATGA CAAAATTTGT GACTCTGACC	360
CTGCTCAGAT GGAGAATATC CGATGTTATC TGCCAGATGC CTATAAGATT ATGTCTCAAA	420
GATGCAATAA CAGAACCCAG TGTGCAGTGG TGGCAGGTCC TGATGTTTTT CCAGACCCGT	480
GTCCAGGAAC CTATAAATAC CTTGAAGTGC AGTATGAATG TGTCCCTTAC ATTTTCTTT	540
GTCTGGACT ACTAAAAGGA GTATACCAGA GTGAACATT GTTTGAGTCC GACCACCAAT	600
CTGGGGCGTG GTGCAAAGAC CCTCTGCAGG CATCTGACAA GATTTATTAT ATGCCCTGGA	660
CTCCCTACAG AACTG	675

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTCGGCC AAAGAGGCCT ACTCCCTGTT TTGAACAAGT TTTTTTGAGA ATTCTTAGTT	60
TTAGTTTTTG TTTAGCTTAC AACTGAAAA TTTTGAGAAG CATCTAAAAA AATCCACAAT	120
TAGTGCAAAA AGAGGGGACA ATACTTTAAG TCATTCCTTC TATAAAAAA ATTAAGGTTA	180
CTAAATGCCA ATTTTTAAGC AAATATATAG TTTCTTATT GCCTTCTGAA AGACAGCAGA	240
TATAAAAAA GTTCAATATT AGGTTTAACA AGGTTTGAAC AACACATGTA CTATCAGCTT	300
TATTTTACCT GCAAAAATAT TTTAGCTACA CTGGAAAAA AATAAACTTG AGAATATAAC	360
TTCACATTC TAAGGCCAGA TGCAAGAATA CTTATTAGG CCTCTTTGGC CGAA	414

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GACCGTCGAT TGAATTCTAG ACCTGCCTCG AGATTGGAGA CAGAAGGTCC CGGGAGCAGA 60  
 AAGCCAAACA GGAGCGGGAG AAAGAACTGG CAAAAGTCAC TATCAAGAAG GAAACTCGAG 120

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTCGGCC AAAGAGGCCT AAGCAGCAGC TGCTTATATG CATGTGAACA GCTGGGGAAT 60  
 TAATTTGGTA TGCATTCTCA GGAGCCACTC ATCTGCTGGC AGAGGTAGCA GAAGAATGCC 120  
 CTTAGTGTA GTCCTCTACA ACCATACACC AAATGTGCTC CCTGCATTTC AAATCCATT 180  
 GTAGAAAGTC TCTGATAATC TCACTTATAC CATGAGCCAT TCCTCAGTAT CTGTCCTCTT 240  
 CCTGTTAGTG TTCTACAATT CCTTCTCCT TAATTTTCT CCGCTTTACA AAATGTCACA 300  
 CAGACAAGTG CATAATACTT AAACAAGCTC GAG 333

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTCGGCC AAAGAGGCCT AAGAAAAGCA CCCTTATTAA GAATTGCAGC AAGTAAGCCA 60  
 ACAAGGTCTT TTCAGGATGA TTTTCTTATA TCAAGTGGTA CATTTTCATT TATTTACTTC 120  
 AGTTTCTGGT GAATGTGTGA CTCAGTTGTT GAAGGACACC TGCTTTGAAG GAGGGGACAT 180  
 TACTACGGTC TTCACACCAA GCGCCAAGTA CTGCCAGGTA GTCTGCACTT ACCACCCAAG 240  
 ATGTTTACTC TTCACTTTCA CGGCGGAATC ACCATCTGAG GATCCCACCC GATGGTTTAC 300  
 TTGTGTCTCG AAAGACAGTG TTACAGAAAC ACTGCCAAGA GTGAATAGGA CAGCAGCGAT 360  
 TTCTGGGTAT TCTTTCAAGC AATGCTCACA CCAAATAAGC GCTTGCAACA AAGACATTTA 420  
 TGTGGACCTA GACATGAAGG GCATAAACTA TAACAGCTCA GTTGCCAAGA GTGCTCAAGA 480  
 ATGCCAAGAA AGATGCACGG ATGACGTCCA CTGCCACTTT TTCACGTACG CCACAAGGCA 540  
 GTTTCCAGC CTGGAGCATC GAAATCTTTG TCTCCTTAAA ACATCTGAGA GTGGATTGCC 600  
 CAGTACACGC ATTAAAAAGA GCAAAGCTCT TTCTGGTTTC AGTCTACAAA GCTGCAGGCA 660  
 CAGCATCCCA GTGTTCTGCC ATTCTTCATT TTACCATGAC ACTGATTCTT TGGGAGAAGA 720  
 ACTGGATATT GTTGCTGCAA AAAGTCACGA GGCTGCCAG AAAGTGTGCA CCAATGCCGT 780  
 CCGCTGCCAG TTTTCTACCT ATACCCCAAC GCTCGAG 817

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```
GAATTCGGCC AAAGAGGCCT AGGAGATACA TCATCATATC ACGGAAAGAG ATGCAGATAG      60
ATCTTTGACC ATACTTGATG AACAGTTATA CTCATTTGCG TTTTCCACCG TGCACATTAC      120
GAAGAAAAGA AATGGAGGTG GGAGTTTAAA TAACTATTCC TCCTCCATTG CATTGACTCC      180
CAGCACCAGC CAGGAGGACC TTTATTTTCAG TGTTCTCTCC ACTGCCAACA CACCCACGCC      240
CGTTTGCAAG CAGTCCATGG GCTGGTCCAA CCTGTTTACA TCTGAGAAAG GGAGTGACCC      300
AGACAAAGGG AGGAAAGCCC TGGAGAGTCA CGCTGACACC ATCGGGAGCG GCAGAGCCAT      360
CCCCATTAAA CAGGGCATGC TCTTAAAGCG AAGTGGGAAA TGGCTGAAGA CGTGGAAAAA      420
GAAATATGTC ACCCTGTGTT CCAATGGCGT GCTCACCTAT TATCAAGCT TAGGTGATTA      480
TATGAAGAAT ATTCATAAAA AAGAGATTGA CCTTCGGACA TCTACCATCA AAGTCCCAGG      540
AAAGTGGCCA TCCCTAGCCA CATCGGCCTG CGCACCCATC TCTCGAG      587
```

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 534 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```
GAATTCGGCC AAAGAGCCTA AGTAGTTGCT GCCTTCTTC AGATCAGGTT ACCACAATGC      60
CTCCCCGCTG CTGACGCTTC ATCCCCACA CCTCCAGCCC CAGTTACCTG GAGCTTCTCA      120
GAACCCACTT TGCCGGTGCT AAAACACAAG AGGGGGTGAA AGTGGCTGCC AGTAATGGCC      180
AGAAACCAAC CACCAGAGGC CAGGCTGAAA GACAAGCTCC GGGTGTCAG GGGCTGACGG      240
GCCAACCATG TGGCAGGTCC CAGGCCCCAC CCACTGCGCC ATCCGTCTCT GAGCTCCACA      300
GTGGTCCCAC TAATGGGAAC CTCCTCTAGG GAGAGTGATA CTGCACCTTC ACCCGTAGGA      360
CTCATATTTA TAACAATGTG TAATGGCTGT AGCAAAAAGC CCTTGTTTCT AGATGTAAAT      420
GGTCAAAGAA ACAAGCGCTC TATTGTTTTG AATAAAATAG TTCAAATGAG TCCTGTATCA      480
TTGTATCTCC TATTCTGGAT TAGTGCCTTT TGGACAGTAG ACTGTAACCT CGAG      534
```

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 118 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```
GCTCCACTCT CTCCCTATCC ATTTGTAAGA ACAGGCTCCC CTCGCCGAAT ACAGTTGTCT      60
CAAAATCATC CTGTCTACAT TTCCCACAT AAAAATGAAA CAATGCTTTC TCCTCGAG      118
```

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```
GAATTCGGCC AAAGAGGCCT AAATTTTAGT AGAGATGGAA TTTCACCATA TTGGCCAGGC      60
CGGTCTCAAA CTCTTGACCT CAAGTGATCT GCCCGCCTCG GCCTCCCAAA ATGTTGAGAT      120
TACAGGCGTG AGCCACCATG CCTCTCTTAC ATTCTTTTCT TCTGTTCACT ACAGCCGTGG      180
AGAGCTCCGG GTTGTCTGTC ACATGTGCAC TGCCCTCTCT TTTATGGACC TTTTAGGCTG      240
GCTGCACCCT CGTCTGTGT CACCCTCCTG CTCCTCCTCC ACCTGGCTAG TTCCTGTTGG      300
CCACTTTTGG AAATTCATGC CAGTCCAGTC CACCCTGAGT ACATCCTCTT TCTGTGTCAC      360
TGAGCTCACT ATGCTGGGTT TTATCTATGT CTCCTCGCA ACTAGATCAT TCAGTCTTG      420
AAGTTAGGCA TCATGCGTTC TTCATTTCTG TACCTCCCAA CTCAATGCTT AGCACCAGC      480
AGGGGCTCAA GACTGTGTGT GGAATGAAGG ATTCGTGTGA AAATGCAGGG AGATGGAAGG      540
CTGAGCGTTT CTGTTCTTG ACCATTCCC GGTGGCTCG AG                          582
```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```
GAATTCGGCC AAAGAGGCCT AAAAATTAT AAATAAGTGA GACTACTGCC CCCTAGCCTA      60
AAATTCATTG CCTGCGCTCA CTCACATCA TAGTCTTTA GGAAGACAAG TTGTTCTATA      120
GCATAAAGAT ACAACCTATT TAGATAGTCT AAAGATTCTC CTCTGTTTCT CAAATACAGT      180
CAGTTATGCA GCTCAAAATG CCTCTCATTT TCCTGCTTTT TTTTCTTCTA CTATTGTTGC      240
CTCCAGGCTT TGCAGAAACA CATGTTATTC TCCCCCTAAA ATCTGTTCTT CTCTAGTTT      300
TCTCTCTGCC AGCAATGGCA CCACACAGTC TTTTGGTTTT GCACCAGAGA ATTAGAGATG      360
AACCCTCAT CTCTAATCTA TCACAAGTTT CCTCAGATTT AAACCTCTCA ATCAAGATGT      420
TTCTACCAT TTCCATTACT ATTGTCCCCA GCTTTCTCGA G                          461
```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```
GCCTAAACCG TCGATTGAAT TCTAGACCTA TCTCGAGAAA GAGTTGTTCT GGAAAGAAAT      60
GAAGAAAAGA GCAGAACCA TCTCAAGCAG CCAAGTGGTG AAGTTGGATG TATGTGACCC      120
TACGTCTCTC GAG                          133
```

(2) INFORMATION FOR SEQ ID NO:229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

GAAAGGGATC AAAAAGAAAA AGTGATCGAA TGGAACTTAC TGATACCAAA CGACAAAAGC      60
CTTCTGTCCA TTCAAGACAA CTGGTTTCTA AGCCACTGAG CTCATCTGTT AGCAATAACA      120
AAAGAATAGT TAGTACAAAA GGAAAGTCAG CCACAGAGTA TAAAAATGAG GAATATCAAA      180
GATCTGAAAG AAACAAGCGT CTAGATGCTG ATCGGAAAAT TCGTCTATCA AGTAGTGCCT      240
CCAGAGAACC TTATAAGAAT CAACCTGAAA AAACCTGTGT CCGGAAAAGG GATCCTGAAA      300
GGAGGGCCAA ATCTCCTACG CCAGATGGTT CTGAGAGAAT TGGGCTTGAA GTGGATAGAC      360
GTGCAAGCAG ATCCAGCCAG TCTTCTAAGG AAGAAGTGAA CTCTGAAGAA TATGGCTCTG      420
ACCATGAGAC TGGCAGCAGT GGTTCCTCTG ATGAGCAAGG GAACAACACT GAAAATCTCG      480
AG

```

## (2) INFORMATION FOR SEQ ID NO:230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

GAATTCGGCC TTCATGGCCT AGGGGATAAA TGTAAGCTTG TTAAAGTAAG CACCACACCA      60
TGTTTCTGTC TCCCAGCAC CCAGCACAGT GCTGTGAACC TTGGCAGATG CTAGATAAAT      120
GTGTGTTGAA TGAATGTGCC TATGAAGCCA CAAAGATGCC ACATGTTAGT ATATCAGTGA      180
GAGGTGACTC CACAGTGCTC TCTGGAGAAG CAATATGAGT GACTGAAGAG TGGGGCCTTT      240
TGCTTTTGCC TGGATATAGG GGTGCTCTTC TACTGTAATT GGGTGTGGAA AAACTCTGGC      300
TTTATGGTAT TCCATTAGGT TCTTTTCATT TAAAGTAGTC TTAAATCAA AGTATCCAAT      360
ATTTTAAAGC CACAAAGTAG ATTACATAAT TAGCAGAGAT TTAGTCAGT AAAATGTTAG      420
AAATCAAAC ATAAAGAAAAT TCAAGTCCTT TATTTTGTGT CTGGGTATA TGTCATTATT      480
TTAAATTCCA CAGCTCTCGA G

```

## (2) INFORMATION FOR SEQ ID NO:231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

GAATTCGGCT TCGATTGAAT TCTAGGACTT GACAGAATTC GAGTTATCCT TCTCAGAACA      60
TGTGCAGAGT CTCTTTTTCG CTCACCATGT GGTCTGTGTC TCTTTCAGGT GGGAGTTTTG      120
GGGCCTCCAG GGCAGCAGGC ACCACCTCCA TATCCCGGCC CACATCCAGC TGGACCCCTT      180
GTCATACAGC AGCCAACAAC ACCCATGTTT GTAGCTCCCC CCCAAAGACC CAGCGGCTTC      240
TTCACCTCAGA GGCCTACCTG AAATACATTG AAGGACTCAG TGCGGAGTCC AACAGCATTG      300

```

CCAAGTGGGA TCAGAGCAAT CTCGAG

326

## (2) INFORMATION FOR SEQ ID NO:232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

GAATTCGGCC TTCATGGCCT AATCAGAAGC TTTTCAAAAT TCCGTCTTCA AGAAGAAACA      60
CCCGTGGAGG AAGAAGACAT TATACAAAAC AAATTTAGAA ACTGGGATCA TGAGTGGAAA      120
AACAAAGGCA AGAAGGGCTG CCATGTTTTT TAGACGTTGC TCTGAAGACG CCAGCGGTAG      180
CGCCAGTGGC AATJCTTTGT TATCAGAGGA CGAAAATCCT GATGCGAATG GGGTAACTCG      240
ATCATGGAAG ATTATTCTAA GTACAATGCT TACACTGACT TTTCTTCTTG TAGGACTCCT      300
AAATCATCAG TGGCTTAAAG AAACAGATGT TCCTCAGAAA TCCAGACAAT TATATGCCAT      360
GCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

GAATTCGGCC TTCATGGCCT AAAGAAGAAT TGACACCTCT TGGAGTCCAC TTGGCAGCAT      60
TACCCGTTGA GCCACATATT GGAAAAATGA TTCTTTTGG AGCACTGTTC TGCTGCTTAG      120
ACCCAGTACT CACTATTGCT GCTAGTCTCA GTTTCAAAGA TCCATTGTG ATTCCACTGG      180
GAAAAGAAAA GATTGCAGAT GCAAGAAGAA AGGAATTGGC AAAGGATACT AGAAGTGATC      240
ACTTAACAGT TGTGAATGCG TTTGAGGGCT GGGAGAGGC TAGGCGACGT GGTTCAGAT      300
ACGAAAAGGA CACACTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

GAATTCGGCT TCATGGCCTA CGATGAGGCT GCTGTCAATTT GTGGTGTGG CTCTATTGTC      60
TGTCACCTCA GCAGAGGAAG GAGCCAGGCT TTTGGCTTCC AAATCACTGC TGAACAGATA      120
CGCCGTGGAG GGACGAGACC TGACCTTGCA GTACAACATC TACAATGTTG GCTCAAGTGC      180
TGCATTAGAC GTGGAATAT CTGATGATTC CTTCCCTCCA GAAGACTTTG GCATTGTGTC      240
TGGAAATGCTC AATGTCAAAT GGGACCGGAT TGCCCTGCT AGCAATGTCT CCCACACTGT      300
GGTCTGCGC CCTCTCAAGG CTGTTTATTT CAACTTCACC TCGGCAACAA TCCTCGAG      358

```

## (2) INFORMATION FOR SEQ ID NO:235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

GAATTCGGCT TCATGGCCTA GTTGACGTA ATGTATTTAT ATGTTAATTT GTTATGTATA      60
TAGATGTGCA AGTCTTGTC AATTTGGCCT CAGTGTAGTT AAAGGGCAGA AGGGGAAGAT      120
ACTGACTAGT CATAGAAATA CCTCATTTCG CTGTGGGAAG AGAAGGGAAG CCCTTTCAGG      180
GTGAGTGAAT GGCAAAGCGG TTGCTTCTGG CTCCTCCTTC CCCTGTGGTC TTGGAAGTGT      240
GTGGAAGGCA GGGACAGAGA TGGAGGCCGA GCCAATAGAC TGAAGAGACC ACAGCAATTG      300
GCTCCTCCAT CTAGAGATTT TCTTGGCAGT ATTCCATGGG ATGTTAAGCA AAGGAAACCA      360
AAGGAATCGT TTCAAATGGA CTCATGGCTT AGAAATCTTT ATTCTTAGGG CAGTCAGTAG      420
TATTCTAAG CTCTCTGACA AGATAAAGGA AGTCACCAA ATTTCTTTT TTAATTGTGA      480
TCTAATCCTC AACAAACAAC CAAACTCTC GAG                                     513

```

## (2) INFORMATION FOR SEQ ID NO:236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

GAATTCGGCC TTCATGGCCT ACTTGGAAT GTTTGATGCT ACTCTGAAAG ATCGAGAACT      60
GAGCTTTCAG TCGGCTCCAG GTACTACCAT GTTCTGTCAT TGGCTAGTGG GAATGGTATA      120
TGTCTTCTAC TTTGCCTCCT TCATTCTACT ACTGAGAGAG GTACTTCGAC CTGGTGTCCCT      180
GTGGTTTCTA AGGAATTGTA ATGATCCAGA TTTCAATCCA GTACAGGAAA TGATCCATTT      240
GCCAATATAT AGGCATCTCC GAAGATTTAT TTTGTCACTG ATGTCTTTG GCTCCATTGT      300
CCTCCTGATG CTTTGGCTTC CTATACGTAT AATTAAGAGT GTGCTGCCTA ATTTCTTCC      360
ATACAATGTC ATGCTCTACA GTGATGCTCC AGTGAGTGAA CTGTCCCTCG AG                                     412

```

## (2) INFORMATION FOR SEQ ID NO:237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

TTCATGGCCT AGAGATATGC TTCTTTGTAC CAATATGGAA AATCTAAAAG AAAAAACCCA      60
CACTCAGCAC TATGAATGTT ATAGGTACCA AAAACTGCAG AAAATGGGCT TTACAGATGT      120
GGGTCCAAAC AACCAGCCAG TTAGTTTTCA AGAAATCTTT GAAGCCAAAA GACAAGAGTT      180
CTATGATCAA TGTCAGAGGG AAGAAGAAGA GTTGAAACAG AGATTATGC AGCGAGTCAA      240
GGAGAAAGAA GCAACATTA AAGAAGCTGA AAAAGAGCTG CAGGACAAGT TCGAGCATCT      300

```